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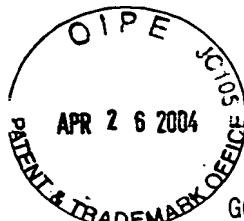
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ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGGCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCGCCGCCCTCCTCCGCCAGGTGTCCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGAAGAACGTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGGACGGGCCGCCGGGGCCCCGAGGCCTTCACCCACCAGCGTGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCACGTGCGGGGAGCGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCGTGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCAGCTGCGCCTACCAGGTGCGGGCCGCCGCTGTACCAAGCTGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCGAAGGCGTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCCTGCCAGCCCCGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCGCGGGGCAGTGCCAGGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240

Fig. 1A



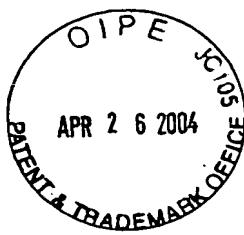
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ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCGCGGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCC	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCCGGTGTACGCCAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCCCAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCAAGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCCGTACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGCCGCCCTGCCTGCCGGCTGGTGCCTGGGCCAGGCTCTGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAAACGAACGCCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500

Fig. 1B



GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTTGGCTG AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	1560 520
CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCCCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
TTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTC PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	1740 580
TGGAGCAAGTTGCAAAGCATTGAAATCAGACAGCACTGAAGAGGGTGCAGCTGCAGGAG TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTCGGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCCGCCCTGCTGACGTCCAGA LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuThrSerArg	1860 620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
GGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	1980 660
CTGTTCAGCGTGCTCAACTACGAGCGGGCGCGCCCGCCTCTGGCGCCTCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	2040 680
CTGGGCCTGGACGATATCCACAGGGCTGGCGCACCTCGTGCCTGCGTGTGCGGGCCAG LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	2100 700
GACCCGCCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTCACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGC ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	2220 740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	2280 760

Fig. 1C



AGCCACGTCTCACCTTGACAGACCTCCAGCCGTACATGCGACAGTCGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTCTCGACGTCTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCCGGGATTGGCGGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	2580 860
GGGCTGCTCCTGCGTTGGATGATTCTTGGTACACCTCACCTCACCCACGCG GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	2640 880
AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGA LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	2700 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAACAGCAGGCCCTGGTGGCACGGCTTTGTT ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	2760 920
CAGATGCCGCCACGGCCTATTCCCTGGTGCAGCCTGCTGGATACCCGGACCCCTG GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuAspThrArgThrLeu	2820 940
GAGGTGCAGAGCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTC GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	2880 960
AACCGCGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGGCTG AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	2940 980
AAGTGTACAGCCTGTTCTGGATTGAGGTGAAACAGCCTCCAGACGGTGTGCACCAAC LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	3000 1000
ATCTACAAGATCCTCCTGCTGCAGCGTACAGGTTCACCGCATGTGTGCTGCAGCTCCCA IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	3060 1020

Fig. 1D



TTTCATCAGCAAGTTGGAAGAACCCACATTTCTGCGCGTACATCTGACACGGCC PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	3120 1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCGAGGATGTCGCTGGGGGCCAAGGGC SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	3180 1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	3240 1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	3300 1100
ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn	3360 1120
CCGGCACTGCCCTCAGACTCAAGACCATCCTGGACTgtatggccacccgcccacagccag ProAlaLeuProSerAspPheLysThrIleLeuAsp	3420 1132
Gccgagagcagacaccagcagccctgtcacgccggctctacgtcccaaggagggaggg Cggcccacaccccgaggccgcaccgtggagctgaggcctgagtgatggccag gcctgcattgtccggctgaaggctgagtgccgtgaggcctgagcgtgtccagccaa ggctgagtgccagcacacccgtccgtttcactccccacaggctggcgctcggtcca ccccagggccagctttccatccaggagccggcttccactccccacatggaaatgg catccccagatttcgcattttccatccggctgcggccctgcggccatccccac catccagggtggagaccctgagaaggaccctggagctctggaaatggagtgacca gtgtgccctgtacacaggcgaggaccctgcacccgtggatgggggtccctgtgg ggggggaggtgctgtggagtaaaatactgaatatatgagttttcagtttggaaaa aaaa	3480 3540 3600 3660 3720 3780 3840 3900 3960 3964

Fig. 1E



Euplotes	1	-----MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSWIWKVIRCR--NQSQSHYKDLEDIK
HT1	1	RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDAR-PPPAAPSFRQVSCLKEVARVQLRLCERGAKNVLAFGFALLGA
EST2	1	-----MKILFEFIQDKLDID--LOTNSTYKENLKCG
Euplotes	56	IFAQTNIVATPRDYNEEDFKVIARK-----EVFSTGLMIELIDKCLVELLSSSDVSDRQKLCQCFGQLKSGNQ-LAK
HT1	80	RGGPPEAFTTSVRSYLPNTVDALRGSGAWGLLRLRVGDDVLVHLLARCALFVLVAPSCAY--QVCGPPLYQLGAAATQA
EST2	30	HFNGLDEILTT-CFALPNSRKIALP-----CLPGDLSHKAVIDHCIYLLTGELYNN--VLTFGYKIARNEDEVNN
Euplotes	126	THLLTALSTQKQYFFQDEWNQVRAMIGNEFRHLYTKYLIFQRTSEGTLVQFCGNVFDHLKVNDKFDKKQKGGAADMNE
HT1	157	RPPPHASGPRRLGGERAWNHSVREAGVPLGLPAPGARRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
EST2	97	SLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQ-FFTQIVGNRCNEPHLPPKWVQRSSSS-----
Euplotes	206	PRCCSTCKYNVKNEKDHLNNI-----NVPNWNMKSRTTRIFYCTHFNRRNNOFF
HT1	237	PSDRGFCVVSARPAEATSLLEGALSGTRHSHPSVGRQHHAGPPSTSRRPPRWDTCPVVAYETKHFYSSGDK--EQLR
EST2	169	-----SATAAQIKQLTEPVTN-----KQFLHKLNIN-SSSFF
Euplotes	255	KKHEFVSNKNNISAM-DRAQTIFTNI-----FRFNIRKKLKDKVIEKIAYMLEVKDFNFNYYLTKSCPLPENWRE
HT1	315	PSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRY-WQMRPLFLELLGNHAQCPYGVLLKTHCPLRAAVTP
EST2	200	PYSKILPSSSSIKKLTDLREAIFP-----TNLVKIPQRLKVRINLTLOKLLKRHKRLNYVSILNSICPPLGET--
Telomerase domain		
Euplotes	326	RK-----QKIENLINKTREEKS--KYYEELFSYTTDNKCVTQFINEFFYNILPKDFLTGR-NRKNFQKKVKKYVELNKHE
HT1	394	AAGVCAREKPQGSVAAPEEEEDTPRRLVQLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNERFLRNTKKFISLGKHA
EST2	268	-----VLDLSHLSRQ-----SPKERVLKFIIVILQKLLPQEMFGSKKNKGKIIKNLNLLSLPLNG
Euplotes	398	LIHKNLLLEKINTREISWMQVET-SAKHFYYFDHENIYVWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYYRKNIW
HT1	474	KLSLQELTWKMSVRDCAWLRRSPGVGCVPAEHRLEEILAKFLHWLMSVYVVELRSFFYVTETTFQKNRLFFYRKSVW
EST2	324	YLPFDSSLKKLRLKDFRWLFISD-IWFTKHNFENLN-QLAICFISWLFRQLIPKIIQTFFYCTEIS-STVTIVYFRHDTW
Motif 1 Motif2		
Euplotes	477	DVIMKMSIADLKK-ETLAEVQEKEVEEWKSL-GFAPGKRLIPKKTT--FRPIMTFNKKIVNSDRK--TTKLTNTKLL
HT1	554	SKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFIPKPDG--LRPIVNMDYVVGARTFRREKRAERLTSRK
EST2	401	NKLITPFIVEYFK-TYLVENNCRNHNSTLS-NFNHSKMRRIIPKKSNNEFRIIAIPCRGADEEEFT--IYKENHKNAIQ

Fig. 2A



Motif A

Euplates 551 NSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQP-KLFFATMDIEKCYDSVNREKLSTFLKTTKLSS
 HT1 632 ALFSVLNYERARR-PGLLGASVLGLDDIHRAWRTFVLVRVRAQDPPPELYFVKVVDVTGAYDTIPQDRLTEVIASIICKPQN
 EST2 477 PTOKILEYLRNKRPTSFTKISPTQIADRIKEFKORLLKKFNNVLP-ELYFMKFDVKSCYDSIPRMECMRILKDALKNEN

Euplates 629 DFWIMTAQILKRKNNIVIDSKNFRKKEMDYFRQKFQKIALEGQQYPTLFSVLENEQNDLNAKKTIVEAK-CRNYFKKD
 HT1 710 TYCVRRYAVVQKAAGHGVRFKAFKSHVS-----TLTDLQPMYRQFVAHLQETSPLRDAVVIQSSLNEASSG
 EST2 556 GFFVRSQYFFN-TNTGVLKLFNVVN-----A-SRVPKPYELYIDNVRTVHLSNQDVINVV-EMEIFKT-

Motif B Motif C

Euplates 708 NLLOPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYyatLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
 HT1 777 LFDVFLRFMCHHAVRIR-GKSYVQCQGIPQGSILSTLLCSLCYQDMEN---KLFAGIRRD-----GLLLRLVDDFLLV
 EST2 616 --ALWVEDKCYIR-----EDGLFQGSSLSAPIVDLVYDDLEFYSEFKASPSQD-----TLILKLAADDFLIIS

Motif D Motif E

Euplates 788 TQENNAVLFIEKLINVSRENGKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIQDYCDWIGISIDMKTALMPNINLRI
 HT1 847 PHILTHAKTFLRTLVRGVPEYGCVVNLRKTVNFPVEDEALGG-TAFVQMPAHGLFPWCGLLDTRTLEVQSDYSSYAR--
 EST2 677 TDQQ-QVINIKKLAMG---GFQKYNAKANRDKILAVS-----SQSDDDTVIQFCAMHIFVKELEVWKSSTMN--

Euplates 868 EGILCTLNLMQTKKASMWLKKKLKSFLMNNITHYFRKTITTEDFANK7LNKLFISGGYKYMQCAKEY--KDHFKKNLAM
 HT1 924 TSIRASLTFNRGFKAGRNMRRKLFGVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVQLPFHQQVWKNPTF
 EST2 741 -----NFHIRSKSS---KGIFRSLIALNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSA--FKDLSINVTO

Euplates 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIEIFSTKKYIFNRVCMILKAKEAKLKSDOCQS
 HT1 1004 FLRVIISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLC-HQAFLLKLTRHRTVYVPLLGSRTAQTQLSRKLP
 EST2 808 NMQFHSFLQRRIEMTVSG---CPITKCDPLIEYEV--FTI--LNGFLESLSNTSKF-KDNIILLRKEIQHLOAYIYI

Euplates 1026 LIQYDA-----
 HT1 1083 TLTALEAAANPALPSDFKTILD
 EST2 879 YIHIVN-----

Fig. 2B

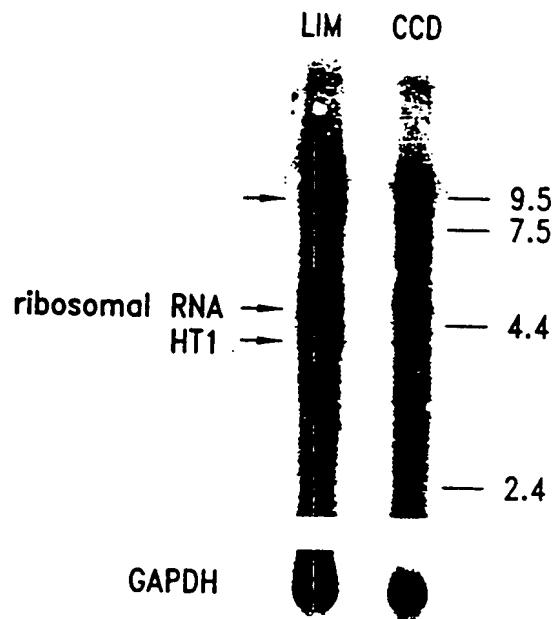


Fig. 3



Plasmid	Human blood				LIM1215							
10	5	1	H	E	P	X	B	H	E	P	X	B

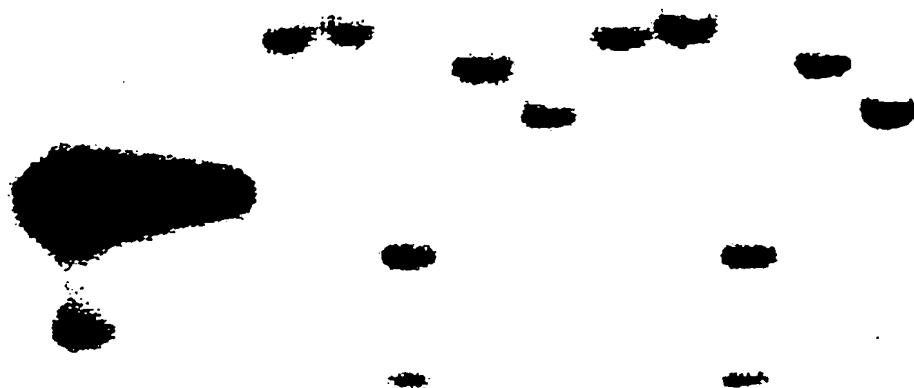


Fig. 4

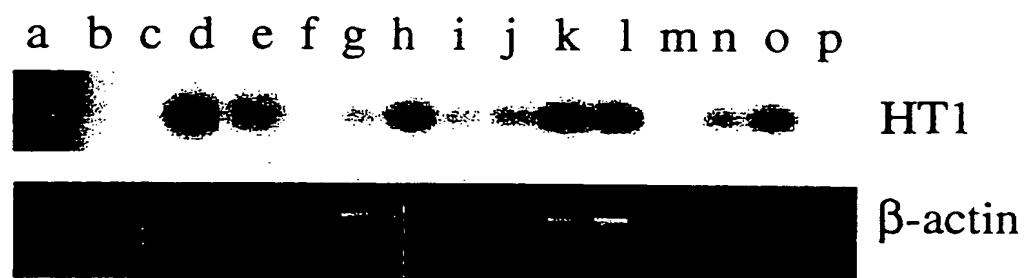


Fig. 5

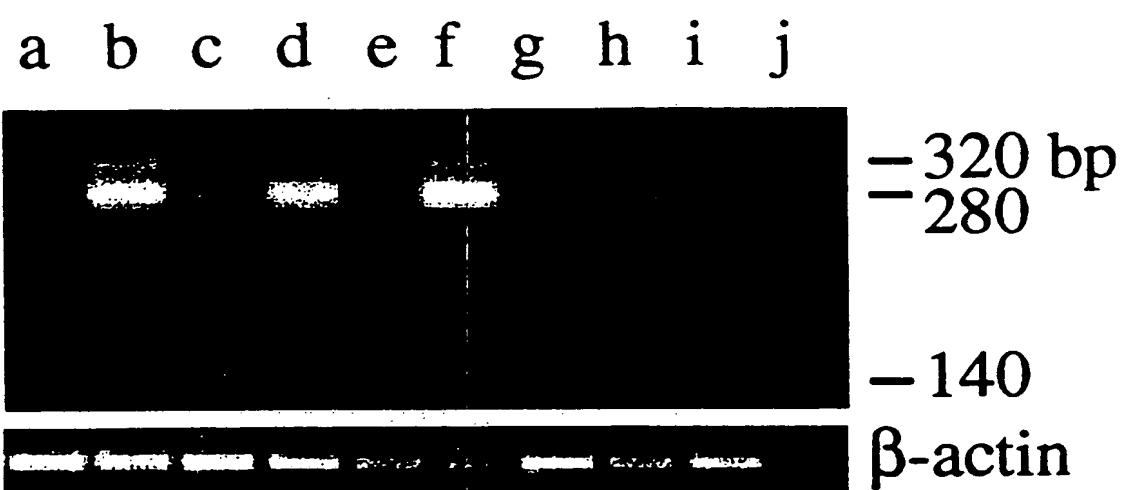


Fig. 6

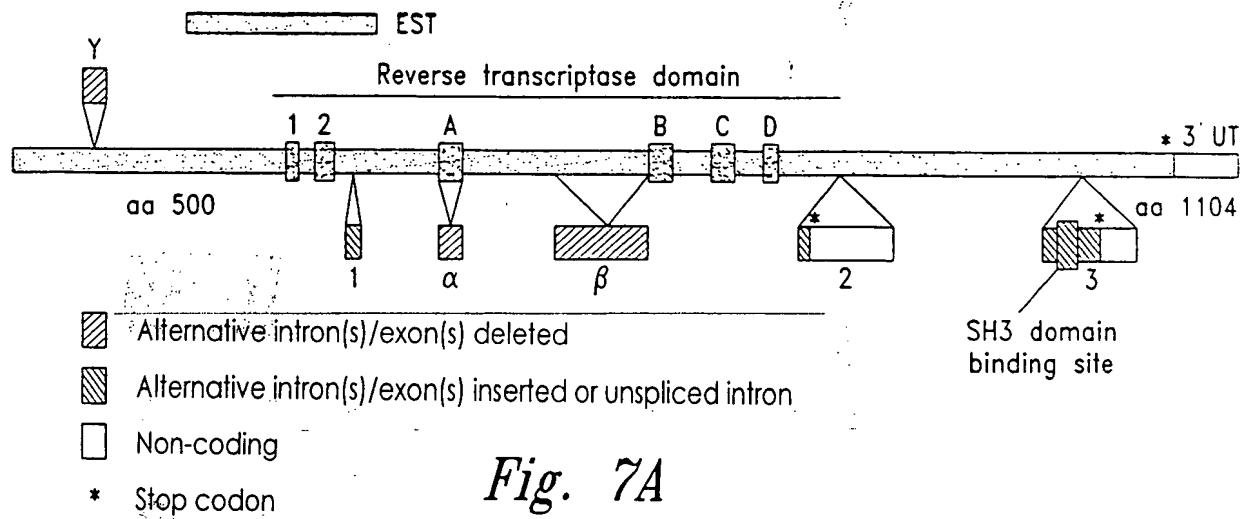


Fig. 7A

Variants:	1	α	β	2	3
RT-PCR product	NO	+	+	NO	+ & -
PCR from LIM1215 lib.	-	+	-	+	NO
RT-PCR product	NO	-	+	NO	+
53.2 cDNA	-	-	-	-	NO

Fig. 7B

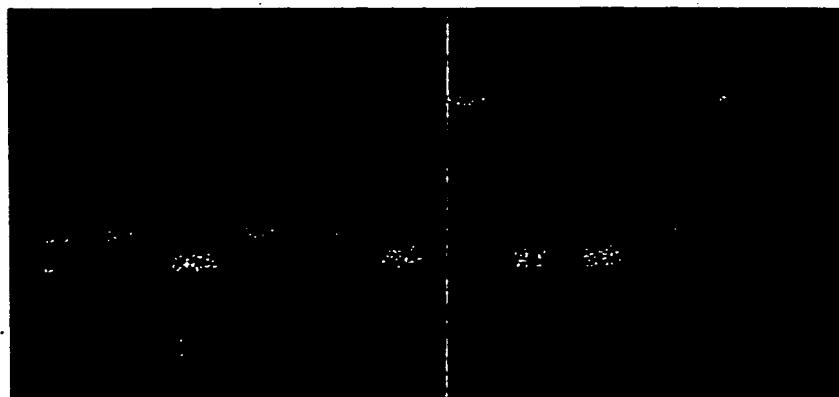


	222	223
Y	5'-CCAGGTG ggcctc	gcaggtg TCCTGCC-3'
	1950	1952
1	5'-AAAGAGG GTGGCTG.....	AACAGAA GCCGAGC-3'
	2130	2167
a	5'-TGTCAAG gtggatg.....	cccccag GACAGGC-3'
	2286	2468
b	5'-GAGCCAC gtctcta.....	ggggcaa GTCCTAC-3'
	2843	2844
2	5'-ACTCCAG GTGAGCG.....	XXXXXXX CTATGCC-3'
	3157	
3	5'-AACGCAG CCGAAGAAAACATTCTGCGTGA	CCTGCCGTGCTGGGTCGGGACAGCCAGAGATGG
	T A A E E N I L V V T P A V L G S G Q P E M E	
	AGCCACCCCGCAGACCGTCGGGTGTGGGCAGCTTCCGGTGTCTCTGGGAGGGGAGTTG	
	P P R R P S G V G S F P V S P G R G V G	
	3158	
	GGCTGGGCCTGTGACTCCTCAGCCTCTGTTCCCCAG GGATGTC-3'	
	L G L *	

Fig. 7C



a b c d e f g h i j k l



- 430 bp
- 400
- 250
- 220

Fig. 8



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTTGCTGCCAGGAGCCAGGGTTGCTGTGTTCCGGCGCAGAGCACCGTCTGGTGAAGGAGATCCTGGCAAGTTCCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGTCAGCTGCTGAGCTGCTCAGGCTTCTTATGTCACGGAGACACGGCTTTCAAAAGAACAGGCTTTCTACCGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGCGGAAGCAGAGGTCAAGCAGCATCGGAAGGCCAGGCCGCGCTGCTACGTCAGACTCCGCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGCGCATTGTGAACATGGACTACGTGCTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGCGCCCCGGCCTCTGGCGCCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCAGCTTGCTGCGTGCGGGCCAGGACCCGGCGCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAGGTTGGATGTGACGGCGCGTACGACACCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCGTATGCCGTGGTCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGCACGTCGCCAAGGCTCAAGAGCCAC
K A A H G H V R K A F K S H

GTCCCTACGTCCAGTG
V L R P V

CCAGGGGATCCCGAGGGCTCCATCCTCTCCACGGCTGCTGAGGCTGTGCTACGGGAGATGGAGAACAGCTGTTCCGGGGATTCCGGGGACGGCTGCTCCGCTTGGTGG
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G

TGATTTCTTGTGGTACACCTCACCTCACCCACGGAAACCTCCTCAGGACCCGGTCCGAGGTGTCCCTGAGTATGGCTCCGTGGTAACCTGGGAAGACAGTGGTAACCTCCC
*

Fig. 11AA



Reference protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGCAGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGGCTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGCCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCGCCGCCAGGTG	
AspAlaArgProProProAlaAlaProSerPheArgGlnVal	
GGCCTCCCCGGGGTCGGCGTCCGGCTGGGTTGAGGGCGGCCGGGGGAACCAGCGACATGCGGAG	
G L P G V G V R L G L R A A G G N Q R H A E	
A S P G S A S G W G * G R P G G T S D M R R	
P P R G R R P A G V E G G R G E P A T C G E	
AGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG	
S S A G D S G R F P R R	
A A Q A T Q G A S P A G	
Q R R R L R A L P P Q V	
TCCTGCCTGAAGGAGCTG	240
SerCysLeuLysGluLeu	80
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTCGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCCTGGACGGGCCCGCGGGGGCCCCCGAGGCCTTCACCACCGCGTGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCGTGGCGACGACGTGCTGGTCACCTGCTGGCACGCTGCGCGCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCAGCTGCGCCTACCAGGTGTGGGGCGCCGCTGTACAGCTCGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCGAAGGCGTCTGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200

Fig. 11AB



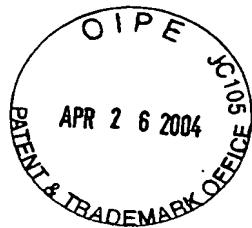
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGCCTGCCAGCCCCGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGCTGGGCCACCCGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTCTGTGTGGTGTACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACACGCCGGCCCCCATCCACATCGCGCCACCACGTCCCTGGGACACGCC	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTCTTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
GTGGAGACCATTTCTGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTGCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
CGCCTGCCCAAGCGCTACTGGCAAATCGGCCCTGTTCTGGAGCTGCTGGAAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCAGGCCGCTGCGAGCTGCCACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCGAGGAG	1320
ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	440
GAGGACACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
GTGTACGGCTTCGTGGGCCCTGCCTGCGCCGGCTGGTCCCCAGGGCTCTGGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTCCTCAGGAACACCAAGAAGTCATCTCCCTGGGGAAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
GCCAAGCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTGGCTG	1560
AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520

Fig. 11AC



CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTACGTCGAGCTGCTCAGGTCTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
TTTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTC PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	1740 580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGCAGCTGCGGGAG TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTCGGAAGCAGAGGTCAAGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCCAGA LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	1860 620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	1980 660
CTGTCAGCGTGCTCAACTACGAGCGGGCGCGCCCGCCCTGCTGGCGCCTCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgProGlyLeuLeuGlyAlaSerVal	2040 680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGTGCGTGTGCGGGCCAG LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	2100 700
GACCCGCCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTCACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGC ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	2220 740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGCACGTCCGCAAGGCCTTCAAG ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	2280 760
AGCCACGTCTCACCTGACAGACCTCCAGCGTACATGCGACAGTTCGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCCCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTTTCGACGTCTCCTACGCTTACATGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCATCCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840

Fig. 11AD



CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGCGGGGATTGGCGGGAC	2580
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	860
GGGCTGCTCCTGCGTTGGATGATTCTTGGTACACCTCACCTCACCCACGCG	2640
GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAACCTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACCTCCCTGAGAACAGCAGGGCCCTGGGTGGCACGGCTTTGTT	2760
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	920
CAGATGCCGGCCCACGGCCTATTCCCTGGTGCAGCCTGCTGGATACCCGGACCCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	940
GAGGTGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCACCTC	2880
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTGGCTG	2940
AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	980
AAGTGTACAGCCTGTTCTGGATTGCAAGGTGAAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCA	3060
IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TTTCATCAGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCATCTGACACGGCC	3120
PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGC	3180
SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	1060
GCCGCCGGCCCTGCCCCTCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC	3240
AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG	3300
LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	1100
ACGCAGCTGAGTCGGAAGCTCCGGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAC	3360
ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAsn	1120
CCGGCACTGCCCTCAGACTCAAGACCACCTGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132

Fig. 11AE



Truncated protein 3 (ver. 2)

ATGCCGCGCCTCCCCCTGCCGAGCCGTGCCCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGCCACGTCGT
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCAGGGCTGGCGCTGGTCACCGCGGGGACCGCGCTTCCGCCGCTGCTGGCCAGTGCCTGGTGTGCCCTGGGACGCACGGCGCCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCGGGTCCGGCTCCGGCTGGGTTGAGGGCGCCGGGGAACCGCAGCATGCCAGAGCAGCAGCGACTCAGGGCGCTCCCCCGAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCTCCGCCAGGTGCTCTGCCCTGAAGGAGCTGGTGCCCCAGTGCTGCAGAGGCTGTGCAGCGCCGGCGAAGAACGTGCTGGCCCTGGCTGCCCTGGACGGGCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACAGCGTGGCAGCTACCTGCCAACACGTGACCGACGCAGTGCAGGGGAGCGGGCGTGGGGCTGCTGCCCTGGCGTGGGACGGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D O V

GCTGGTTACCTGCTGGCACGCTGGCGCTCTTGCTGGCTCCAGCTGCCCTACCGGTGCTGGCCGCGCTGTACCACTGGCGCTGCCACTCAGGGCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCCTGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGGCTCCCTGGCCTGCCAGCCCCGGTGCAGGGAGGCCTGGGAG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CACCGAAGTCTGCCCTGCCAACAGGGCAGGCCAGGTGGCGCTGCCCTGAGCGAGCGAGCCGGTGGCAGGGGCTGGCCACCCGGCAGGACCGTGGACCGAGTGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTTGCTCACCTGCCAGACCCGCCAGAACAGGCCACCTCTTGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTGGCCGCCACACGCCGGGGGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCAACACGCCCTGGACACGCCCTGGTACGCCAGACCAAGCCTCCCTACTCCCTAGCGACAAGGAGCAGCTGCCCTCCCTACTCG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L S

CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGTGCCTACGGGGTCTCTCAAGACGCACTGCCCTGCCAGCTGCCAGGCCGTCTGTGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAACCCAGGGCTCTGCGGCCCGAGGAGGGACACAGACCCCCCTGCCCTGGTGCAGCTGCCAGACAGCAGCCCTGGCAGGTGACGGCTCTGCGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTGGCCCTGCCAGGCACACGAACGCCCTCTGGGCTCAGGCACACGAACGCCCTCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L O E L

Fig. 11AF



GACGTGGAAGATGAGCGTGGGGACTGCGCTGGCTGCGCAGGAGCCCAGGGGTTGGCTGTTCCGGCCAGAGCACCGCTCGCTGAGGAGATCTGGCAAGTTCTGCACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGTCAGCTGCTCAGGTCTTCTTATGTCACGGAGACCACTTCAAAAGAACAGGCTTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGCGGAAGCAGAGGTCAAGCAGCATCGGAAGGCCAGGCCCTGCTGACGTCAGACTCCGCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTGGCCGATTGTGAAACATGGACTACGTCGTCGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTAAGGCAGTGTCTAGCTGCTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGCCGCCGGCCTCTGGCGCCTCTGTGCTGGCCTGGACGATATCCACAGGGCTGGCGACCTCGTGTGCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAGGTGGATGTGACGGCGCGTACGACACCATCCCCAGGACAGGCTACGGAGGTCACTGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGAGCTGTACTT
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCCGCCATGGCACGTCGCAAGGCCCTCAAGAGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCCAGCAGTCAGTTGCTGGCTCACCTGCAAGGAGACCAGCCGCTGAGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGCTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCTCTTGACGCTTCTACGCTTATGTGCCACACGCCGTGCATCAGGGCAAGTCCACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTGACGCCCTGCTACGGGACATGGAGAACAGCTGTTGCGGGATTGCGGGACGGCTGCTCTGCGTTGGTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R O G L L L R L V D

TGATTTCTGTTGGTACACCTCACCTCACCCACCGAAAACCTTCCTCAGGACCCCTGGTCCAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGCGGAAGACAGTGGTAACCTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGAGAAGACGAGGCCCTGGTGGCACGGCTTGTAGATGCCGCCACGCCATTCCCTGGTGCCTGCTGGATAACCCGACCCCTGGAGGTGAGAGCAGACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCGCACCTGGCGGAAGTGGAGCCGTGCCCCGGCTGGGCAAGGTGCTGCTGCAAGGCCCTTGGTCCACCTCTGCTTCCGTGTGGCAGGCAGTCCAATCCAAAGGGTCAAGA
*

TGCCACAGGGTCCCCCTCTCCATCTGGGCTGAGCACAAATGCATTTCTGTTGGAGTGAGGTGCTCACACGGAGCAGTTCTGTGCTATTTGGTAA.....

Fig. 11AG



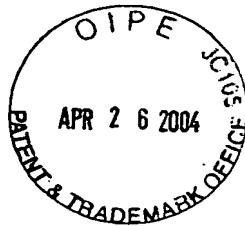
Altered C-terminus protein (ver. 2)

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGTCCTGCTGCCAGGCCACTACCGCGAGGTGCTGCCGTGGCACGTTGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCCGCTGGTGGCCAGTGCCTGGTGTGCCGTGCCCTGGGACGCACGGCCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCGGGTCCGGCTGGTGGGGTAAGGGCGCCGGGGAAACAGCGACATGCCAGAGCAGGCCAGGCGACTCAGGGCGCTCCCCCGAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V
|.
CCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCTTCGGCTCGCCTGCTGGACGGGCCG
P S F R Q V S C L K E L V A R V L O R L C E R G A K N V L A F G F A L L D G A R
CGGGGGCCCCCGAGGCCCTCACCAACAGCGTGCAGCTACCTGCCAACAGGTGACCGACGCACGCCGGGAGCGGGCGTGGGGCTGCTGCCCGCGTGGCGACGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V
GCTGGTTACCTGCTGGCACGCTGGCGCTTTGTGCTGGTCCAGCTGCCAACAGGTGACCGACGCACGCCGGGAGCGGGCGTGGGGCTGCTGCCCGCGTGGCGACGACG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P
ACACGCTAGGGACCCGAAGGGCTGGGATGCAACGGCCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCTGGCCTGCCAGCCCCGGTGGAGAGGCCGGGGCAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A
CAGCCGAAGCTGCCGTTGCCAACAGGGCCAGGCGTGGCGCTGCCCTGAGCCGAGGCCGAGGGCTGGCAGGGCTGGGCCACCCGGCAGGACCGCTGGACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R
TGGTTCTGTTGGTGTACCTGCCAGACCCGCCAACGACCTCTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGCCAGCACACGCCGGGGGGGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P
ATCCACATGCCGCCACCGCTCCGGACACGCCCTGGTACGCCAGACCAAGCCTCCCTACTCCAGGCCACAAGGAGCAGCTGCCCTCCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S
CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q
AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGCGAGCTGCCCTACGGGGTGCCTCAAGACGCACGCCCTGCCAGCTGCCAGGCCAGCGCTACTGGCA
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R
GGAGAACCCAGGGCTCTGGCGGCCCGAGGAGGAGCACAGACCCCGTCCCTGGTGCAGCTGCCAGCACAGCAGCCCTGGCAGGTACGGCTCGCAGGGCT
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C
CTGCCGCCCTGGTCCAGGCCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAGCTCGCAGGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AH



GACGTGGAAGATGAGCGTGGGACTGGCCTTGGCTGCGCAGGAGCCAGGGTGGCTGTTCCGGCGAGAGCACCGTCTGCGTGGAGAGATCTGGCAAGTTCTGCACTGGCT
TWKMSVRDCAWLRRSPGVGCVPAAEHRLREELAKFLHWL
GATGAGTGTGACGTCGTCAGCTCTTCTTATGTACGGAGACACGTTCAAAAGAACAGGCTTTCTACCGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLOQSIG
AATCAGACAGCACTTGAAGAGGGTGCAGCTCCGGAGCTGCGAAGCAGGGTCAGGAGCATCGGAAGCCAGGCCCTGCTGACGTCCAGACTCCGTTATCCCCAAGCCTGA
IRQHLKRVQLRELSEAEVROHREARPALTSRLRFIPKPD
CGGGCTGCGCCGATTGTGAAACATGGACTACGTGTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGGGTCACTCGAGGGTAAGGCACTGTCAGCGTCTCAACTACGA
GLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYE
GCGGGCGGGCGCCCCGGCTCTGGCGCTCTGTGCTGGCCTGGACGATATCCACAGGGCTGGGCACCTCGTGTGCGTGTGCGGCCAGGACCCGCCGAGCTGACTT
RARRPGELLGASVLAGLDDIHRAWRTFVLRVRAQDPPPELYF
TGTCAAGGTGGATGTGACGGCGCTACGACACCATCCCCAGGACAGGTCACGGAGGTACGCCAGCATCATCAACCCAGAACACGTACTCGTGTGCGTGTGCGTATGCCGTG
VKVDVTGAYDTIPQDRLTEVIASIICKPQNTYCVRRYAVVQ
GAAGGCCCATGGCACGTCGCAAGGCCCTCAAGAGCCACGCTCACCTGACAGACCTCCAGCGTACATGCCAGCATCGCACAGTTCGTTGCTCACCTGCAGGAGACAGCCGCTGAGGGA
KAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD
TGCCGTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTCTACGCTCATGTGCCACCACGCCGCGCATCAGGGCAAGTCAGTCAGTG
AVVIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQC
CCAGGGATCCCGCAGGGCTCCATCTCCACGCTCTGAGCCGACATGGAGAACAGCTGTTGGGGATTGGCGGGACGGCTGCTCTGCCTTGGGA
QGIPQGSILSTLCSLCYGDMEENKLFAGIRRDOGLLLRLVD
TGATTTCTTGTGGTGAACCTCACCTCACCGAAAACCTCTCAGGACCTGGTCCAGGAGCTGAGTATGGCTGCTGGTAACCTGCCAGAGCAGTGGTAACCTCC
DFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNF
TGTAGAAGACGAGGCCCTGGTGGCACGGCTTGTCAAGATGCCGCCACGGCTATTCCCTGGTGGCGCTGCTGGATACCGGACCCGGAGGTGCAAGCGACTACTCCAG
VEDEALGGTAFVQMPAHGLFPWCGGLLDTRTLEVQSDYSS
CTATGCCGACCTCCATCAGAGCCAGTCACTCAACCGGGCTCAAGGCTGGAGGAACATGCCAGAACACTTGGGCTTGGCTGAAGTGTCAAGCCGTTCTGG
YARTSIRASLTNFNRGFKAAGRNMRRKLFGVRLRKCHSLFLD
TTTGCAGGTGAACAGCCTCACAGGGTGTGACCAACATCTACAAGATCTCTGCTGAGGTTCACGCCATGTGCTGAGCTCCATTCTACAGCAAGTTGGAGAA
LQVNSLQTVCTNIYKILLLQAYRFHACVLLQLPFHQQVWK
CCCCACATTTCTGCGCTCATCTGACACGGCTCCCTGCTACTCCATCTGAAAGCCAAGAACGCCAGGGATGCTGGGGCCAAGGGCGCCGCCCTGCTGCCCTCCGA
PTFFLRLVISDTASLCYSILKAKNAE
|
CCGAAGAAAACATTCTGCTGACTCTGGCTGCTTGGGTC
EENILVVTPAVLGS
GGGACAGCCAGAGATGGAGCCACCCCGCAGACCGTCGGGTGAGCTTCCGGTCTCTGGAGGGAGTTGGCTGGGCTGTGACTCTCAGCCTCTGTTCCCCAG
GQPEMEEPRLRPSGVGSFPVSPGREGVGLGL*

Fig. 11AI



Protein that lacks motif A (ver. 2)

ATGCCGCCGCTCCCCCTGCCAGGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTTCTG
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

 CGGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCCGGGGACCCGGCGCTTCCGCCGCTGGTGGCCAGTGCCTGGTGTGCCTGGGACGCCACGGCCGCCCCCGCCG
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

 GGCTCCCGGGTCGGCGTCCGGCTGGGTGAGGCCGGGGGGAAACAGCAGCATGCCAGAGCAGCGCAGGCAGCTCAGGGCCTCCCCCGCAGGTG
 G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

 CCCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCGAGTGCAGAGGCTGTGCAGCGCAGCGAAGAACGTGCTGGCCTCGGCTGCTGGACGGGCCCC
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

 CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCAGCAGCTGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCGCGTGGCGACGAGT
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

 GCTGGTTCACCTGCTGGCACGCTGCCCTTTGTGCTGGCTCCAGCTGCCCTACCGGTGCTGCCCTACCGAGCTGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCGCGTGGCGACGAGT
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

 ACACGCTAGTGGACCCGAAGGGCTGGGATGCGAACGGGCTGGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGGCTGCCAGCCCGGGTGCAGGGAGGCCGGGAGCTGC
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

 CAGCCGAAGTCTGCCGTGCCAAGAGGCCAGGCCTGGCGCTGCCCTGAGCCGAGCCGACGCCGTTGGCAGGGCTGGGCCACCCGGCAGGACGCGTGGACCGACTGACCG
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

 TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAGAACGCCACCTCTTGAGGGTGCCTCTGGCACGCCACTCCACCCATCGTGGGCCAGCACCGGGCCCC
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

 ATCCACATCGGGCCACACGCTCCCTGGACACGCCCTGTCCCCCGTACGCCAGACCAAGCAGCTCTACTCTCAGGCAGCAAGGAGCAGCTGCCCTCTTCTACTCAG
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

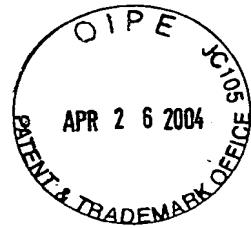
 CTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTGGAGACCATCTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGGCCACTGGCA
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

 AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGCGCAGTGCCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCAGGCCAGGCCAGGCCAG
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

 GGAGAAGCCCAAGGGCTGTGGCGCCCCAGGCCTCTGGGCTCCAGGCACAACGAACGCCCTGCCAGGAGGACACAGACCCCGTCGCTGGTCAAGCAGGCCCTGGCAGGTGACGGCTCGTGGGGCTG
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

 CCTGCCGGCTGGTGGCCCTGCCAGGCCTCTGGGCTCCAGGCACAACGAACGCCCTGCCAGGAGGACACAGACCCCGTCGCTGGTCAAGCAGGCCCTGGCAGGTGACGGCTCGTGGGGCTG
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AJ



GACGTGAAAGATGACGCTGGGGACTGCCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGCCAGACCCGCTGGTGGAGATCTGCCAAGTCCGACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L
GATGAGTGTGACGCTGAGCTGCTCAGGCTTTATGTACGGAGACACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTGGACCAAGTTGCAAACCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
AATCAGACAGCACTTGAAGAGGGTGAGCTGCCAGCTGAGGTCAGGCAGCATCGGAAGCCAGGCCGCTGACGTCAGACTCCGTTATCCCAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGCCGCCATTGTGAACATGGACTACGTCGAGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGCTCACCTCGAGGGTAAGGCAGTGTACGCTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGCGCCGCCGCCGCCCTCTGGGCCCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTCGTGTGCGTGGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAG GACAGGCTACGGAGGTACGCCAGCATCATCAAACCCAGAACACGTAACGCTGCGTGCCTGATGCCGTGGCAACTACGA
V K D R L T E V I A S I I K P O N T Y C V R R Y A V V Q
GAAGGCCCATGGCACGCTCGAAGGCCACGCTCTACCTGACAGACCTCCAGCGTACATGCGACAGTGTGGCTACCTGCAGGAGACGCCGCTGAGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGTCGTCATGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTCTCGACGCTTACGCTCATGTGCCACACGCCGCGCATCAGGGCAAGTCCACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCCGCAGGGCTCATCCTCTCCACGCTGCTGAGCCGACATGGAGAACAGCTGTTGGGATTCGGGGACGGCTGCTCTGCCTGGTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D
TGATTCCTGGTGAACCTCACCTCACCGAAAACCTCTCAGGACCTGGTGGAGGTCTCTGAGTATGGCTGCGTGGTAACCTGGGAAGACAGTGTGAACCTCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGAGAAGACGAGGCCCTGGTGCACGGCTTCTGAGATGCCGCCACGGCTATTCCCTGGTGGCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S
CTATGCCGACCTCCATCAGAGCCAGTCTACCTCAACCGCCCTCAAGGCTGGAGAACATGCGTCGAAACTCTTGGGCTTGGCTGAAGTGTACAGCTGTTGG
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D
TTGCAGGTGAACAGCCTCACAGCGTGTGACCAACATCTACAAGATCCTCTGCTGCAGGGTACAGTTACGCATGTGCTGCAGCTCCATTTCATCAGCAAGTTGGAAAGAA
L Q V N S L Q T V C T N I Y K I L L Q A Y R F H A C V L Q L P F H Q Q V W K N
CCCCACATTTCTGCGCTCATCTGACACGGCTCCCTGCTACTCCATCTGAAGCCAAGAACGAGGGATGCGCTGGGGCAAGGGGCCGCGCCCTGCCCCTCGA
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E
GGCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTCACTACGTCACCTGGGACTCAGGACAGCCAGACGAGCTGAGTCGGAAGCTCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P
GGGAGACGCGTGAATGCCCTGGAGGCCAGCCAACCCGGACTGCCCTGACTCAAGACCATCTGGACTGATGCCACCCGCCACAGCCAGGCCAGAGCAGACACCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D

Fig. 11AK



CTGTCACGCCGGCTCACGTCCCAGGGAGGGAGGGCGGCCACACCCAGGCCCGCACCGCTGGAGTCTGAGGCCCTGAGTGACTGTTGGCCGAGGCCCTGCATGTCCGGCTGAAGGCT
GAGTGTCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCAGCACCTGCCCTTCACCTCCCCACAGGCTGGCGCTGGCTCCACCCAGGGCCAGCTTCCCTCAC
CAGGAGCCCGCTCCACTCCCCACATAGGAATAGTCATCCCCAGATTGCCATTGTTACCCCTGCCCTGCCCTCCACCCACCATCCAGGTGGAGACCCCTGAGAA
GGACCCCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCAGGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGGAGTAA
AATACTGAATATGAGTTTCAGTTTGA

Fig. 11AL



Truncated protein that lacks motif A (ver. 2)

ATGCCGCGCCTCCCCCTGCCAGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTTCTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGGCCCAGGGCTGGCGCTGGTGCAGCGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGGACGACGGCCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCGGGTGGCGTCCGGCTGGGTGAGGCGCCGGGGAAACAGCAGCATGCGAGAGCAGCGCAGGCAGTCAGGGCCTCCCCCGAGGT
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCAGAGGCTGTGCAGCGCGCGAAGAACGTGCTGGCCTCGGCTCGCCTGCTGGACGGGCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACCGTACCGCAGCAGTGGGGAGCGGGCTGGGGCTGCTGCAGCCGCGTGGCGACGAGCT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACGCTGCCTCTTGCTGGCTCCAGCTGGCCCTACAGGTGCGGGCCCGCTGTACAGCTGGCCTGCCACTCAGGCCGGCCCCCG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGCCTGGGATGCAACGGCCCTGGAACCATAGCGTCAAGGAGGCGGGTCCCTGGCCTGCCAGCCCAGGTGCGAGGAGGCGGGCAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCCTGCCAACAGGCCAGGCCTGGCGCTGCCCTGAGCCAGCGAGCCCTGGCAGGGCTCTGGCCACCCGCCAGGACGCGTGGACCGAGTC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCCGGAAGAAGCCACCTTTGGAGGGTGCCTCTGGCACCGCCTACTCCACCCATCCGTGGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCAACACGCTCCGGACACGCCCTGGTACGCCAGACCAAGCCTCTGGAGGGTGCCTCTGGCACCGCAGTCAGGCAAGGAGCAGCTGCCCTCCCTACTCAG
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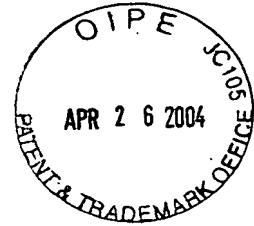
CTCTCTGAGGCCAGCCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACACCGCAGTGCCTACGGGTGCTCCCAAGACGCACTGCCGCTGCCAGCTGCCAGCAGCCAGGTGCTGTGCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGGCCAGGGCTGTGGCGCCCCAGGCCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAACCTCGCAGGAGCT
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P H Q V Y G F V R A C

CCTGCCGCCCTGGTGCCTGGGCCAGGCCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAACCTCGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11AM



GACGTGGAAAGATGAGCGTGGGGACTGGCCTGGCTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCAGAGCAGCGTCTGGCTGAGGAGATCTGGCAAGTTCTGCACGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L
GATGAGTGTGTACGTCGTCAGCTGCTCAGGCTTTATGTACGGAGACACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
AATCAGACAGCACTGAAGAGGGTGCAGCTGGGGAGCTGTCGGAAGCAGAGTCAGGCAGCATGGGAAGCCAGGCCGCTGCTGACGTCCAGACTCCGTTATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGCGGCCATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGGGCTCACCTGAGGGTAAGGCAGTGTCAAGCTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GCGGGCGGGCGCCCCGGCTCCTGGGCGCTCTGTGCTGGGCTGGACGATATCACAGGGCTGGCGACCTCTGCTGCGTGTGCGGGCCAGGACCCGCCGCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTAACGCTGCGCTCGGTATGCCGTGGCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCCCCCATGGCACGTCGCAAGGCCACGTCACCTGACAGACCTCCAGCGTACATGCGACAGTTGCTGGCTACCTGCAGGAGACAGCCGCTGAGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCCGTGTCATCGAGCAGACTCTCCCTGAATGAGGCCAGCAGTGGCTCTGACGCTTCTACGCTTATGTGCCACACGCCGCGCATCAGGGCAAGTCTACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGCTACGGCAGATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCGTTGGTGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D
TGATTCTTGTGGTACACCTCACCTCACCCACGGAAAACCTTCCTCAGGACCTGGCTGAGTATGGCTGCGTGGTAACCTGCGGAAGACAGTGGTAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGAGAACGAGGCCCTGGTGGCACGGCTTGTAGATGCCGCCACGGCTATTCCCTGGTGGCTGCTGGATAACCCGACCCGGAGGTGAGAGCAGACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R
GTGAGCGCACCTGGCCGGAAAGTGGAGCCGTGCCCCGGCTGGGAGGTGCTGCTGAGGGCCCTGGTCCACCTCTGCTTCCGTGCGGGCAGGGACTGCCAATCCCCAAGGGTCAGA
*
TGCCACAGGGTCCCCCTGTCATCTGGGCTGAGCACAAATGCATTTCTGTTGGAGTGAGGGTGCTCACACGGAGCACGTTCTGCTATTTGGTAA.....

Fig. 11AN



Lacks motif A and altered C-terminus (ver. 2)

ATGCCGCGCCTCCCCGTGCCAGGCCGTGCCCTGCTGCCAGCCACTACCGGAGGTGCTGCCGTGCCACGTC
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

 CGGCCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGGGACGCACGGCCGCCCCCGCCG
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

 GGCCTCCCGGGTCCGGTGGGGTGGGGGAAACAGCCACATGCCAGAGCCAGCGACTCAGGGCCTCCCCGAGGT
 G L P G V G V R L G L R A A G G N O R H A E S S A G D S G R F P R R
 A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
 P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

 CCCCTCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCGAGTGCTGCCAGGGCTGCGAGCCGGCGCAAGAACGTCGCTGGCTTCGGCTCGGCTGCTGGACGGGCCCC
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

 CGGGGGCCCCCGAGGCTTACCCACAGCGTGGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGGGGGCTGGGGCTGCTGCTGCCCGGCTGGCGACGCT
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

 GCTGGTTCACCTGCTGGCACGCTGCCGCTTTGTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCGCTGTACCGCTGGCCGCTGCCACTCAGGCCGGCTGGCGACGCT
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

 ACACGCTAGTGGACCCGAAGGCCTGGGATGCCAACGGCCCTGGGACCGCACAGCGTCAAGGAGGGCCGGTCCCTGGGCTGCCAGCCCGGGTGCAGGGAGGGCGAGCT
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

 CAGCCGAAGTGTGCCCTTGCCTGAAGAGGCCAGGCCTGGCGCTGCCCTGAGCCGAGGCCGCTGGGAGGGCTGGGAGGGCTGGGAGGGCCACCCGGCAGGACGCGTGGACCG
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

 TGGTTCTGTGGTGTACCTGCCAGACCCCGAAGAAGCCACCTCTTGAGGGCTGGCTCTGGCACGCCACTCCACCCATCCGTGGCCGAGCACACCCGGCC
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R O H H A G P P

 ATCCACATGCCGCCACACGCCCTGGACACGCCCTGTCCCCGGTACGCCAGACCAAGCCTCCCTACTCCCTAGCGACAAGGAGCAGCTGCCCTCCCTACTCAG
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

 CTCTCTGAGGCCAGCCTGACTGGCCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTTGCCCTGCCAGCGTACTGGCA
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

 AATGCCGCCCTGTTCTGGAGCTGCTGGGACACGCCAGCGAGCTGCCCTACGGGTGCTCTCAAGACGCACTGCCCTGCCAGCTGCCAGCGTACCCAGCAGCCGTGTGCC
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

 GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGAGGAGCACAGACCCCGTCGCTGGAGCAGCACAGCAGCCCTGGCAGGTGACGGCTCGTGCAGGCT
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

 CCTGCGCCGGCTGGTGCCTGGGCTCCAGGCACAACGAACGCCGCTCTCAGGAACACCAAGAAGTCATCTCCCTGGGAGCATGCCAGCTGCCAGGAGCT
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S I Q E L

Fig. 11AO



GACGTGGAAGATGAGCGTGGGGACTGGCTGGCTGCGCAGGAGCCAGGGGTGGCTGTTCCGGCCAGAGCAGCGTCTGCGTGAAGGAGATCCTGGCCAAGTTCTGCACTGGCT
THKMSVRDCAWLRRSPGVGCVPAAEHRLREELAKFLHWL
GATGAGTGTGACGTCGCTGAGCTGCTCAGGCTTTCTTATGTCACGGAGACACGTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG
MSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLOQSIG
AATCAGACAGCACTGAAGAGGGTGCAGCTGGGGAGCTGTCGAAGCAGAGGTCAAGCAGCATCGGAAGGCCAGGCCGCTGCTGACGTCCAGACTCCGTTCATCCCAAGCCCTGA
IRQHLKRVQLRELSEAEVROHREARPAALLTSRLRFIPKPD
CGGGCTGGGCCATTGTGAACATGGACTACGTCGCGAGCCAGAACGTTCCGAGAGAAAAGAGGCCAGGGCTCACCTCGAGGGTAAGGCAGTGTCAAGCTGCTCAACTACGA
GLRPIVNMDYVVVGARTFRREKRAERLTSRVKALFSVLNYE
CGGGGCGGGCGCCCGGCCCTGGGCCCTGTGCTGGGCCCTGGACGATATCACAGGGCCTGGCACCTCGTGTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGACTT
RARRPGLLGASVLDODIHRAWRTFVLRVRAQDPPPPELYF
TGTCAAG GACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTCGTGCCTGGTATGCCGTGCA
VK DRLTEVIASIIKPQNTYCVRRYAVVQ
GAAGGCCCCCATGGCACGTCGCCAAGGCCACGTCACCTGACAGACCTCCAGCTACATGCCAGCTGGCTCACCTGAGGGACCCGCTGAGGAGAACAGCCGCTGAGGA
KAAGHGHVRKAFKSHVSTLTDLOPYMRQFVAHLOETSPLRD
TGCCGTCGTCATCGAGCAGAGCTCCCTCCCTGAATGAGGCCAGCAGTGGCTCTTGACGTTCTACGTTCATGTGCCACACGCCGTGCGCATCAGGGCAAGTCTACGTCAGTG
AVVIEQSSSLNEASSGLFDVFLRFMCHHAVERIRGKSYVQC
CCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGAGCTGGCAGATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCGTTGGGGA
QGIPQGSILSTLLCSLCYGDMEENKLFAAGIRRDGLLLRLVD
TGATTCTTGTGGTACACCTCACCTCACCCACGCCAAAACCTTCCTCAGGACCTGGTCCAGGAGGTGTCCTGAGTATGGCTGCGTGGTAACCTGGGAAGAACAGTGGTAACCTCC
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EENILVVTPTPAVLGS
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Fig. 11AP

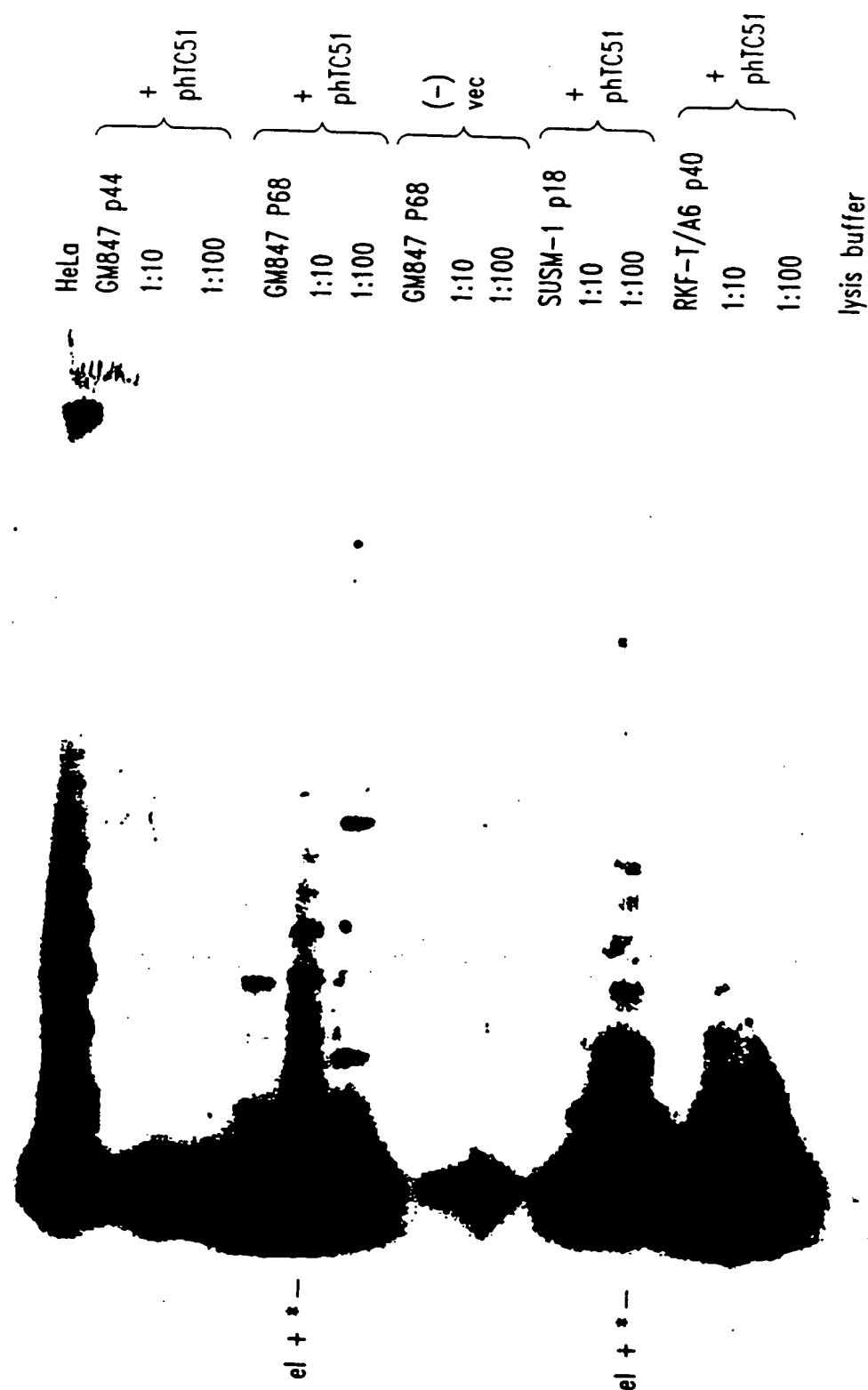


Fig. 12

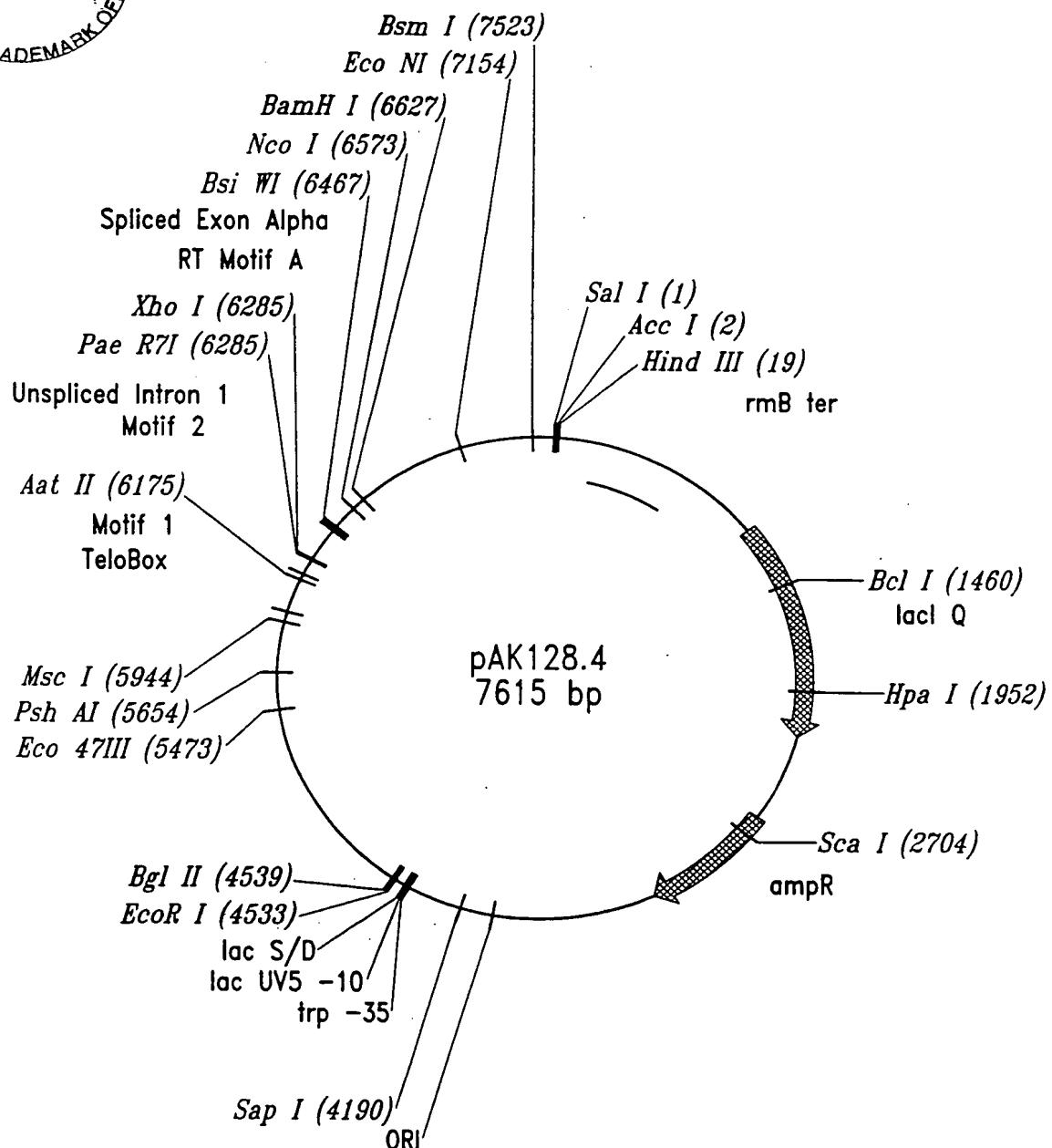
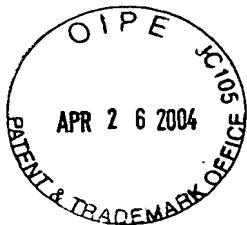


Fig. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular
DEFINITION Human telomerase clone with exon beta spliced out



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61 aaccctggcg ttacccaact taatcgccct gcagcacatc ccccttcgc cagctggcg
121 aatagcgaag aggccccgac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa
181 tggccctgaa tgcgttattt tctccttacg catctgtgcg gtatttcaca ccgcataat
241 tccctgtttt ggcggatgag agaagattt cagcctgata cagattaaat cagaacgcag
301 aagggtctg ataaaacaga atttgcctgg cggcagtagc gccgtggcc cacctgaccc
361 catgccgaac tcagaagtga aacgcgttag cgccgtatgtt agtgtgggtt ctccccatgc
421 gagagttaggg aactgccagg catcaaataa aacgaaaggc tcagtcgaaa gactgggcct
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1261 tggccggccaa acagtcgtt ctgattggcg ttgccaccc cagtctggcc ctgcacgcgc
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2581 aacgtttcc aatgtatggc actttaaag ttctgtatg tggccggta ttatcccgt
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Fig. 13B



2701 agtactcacc agtcacagaa aagcatctta cgatggcat gacagtaaga gaattatgca
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Fig. 13C



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Fig. 13D

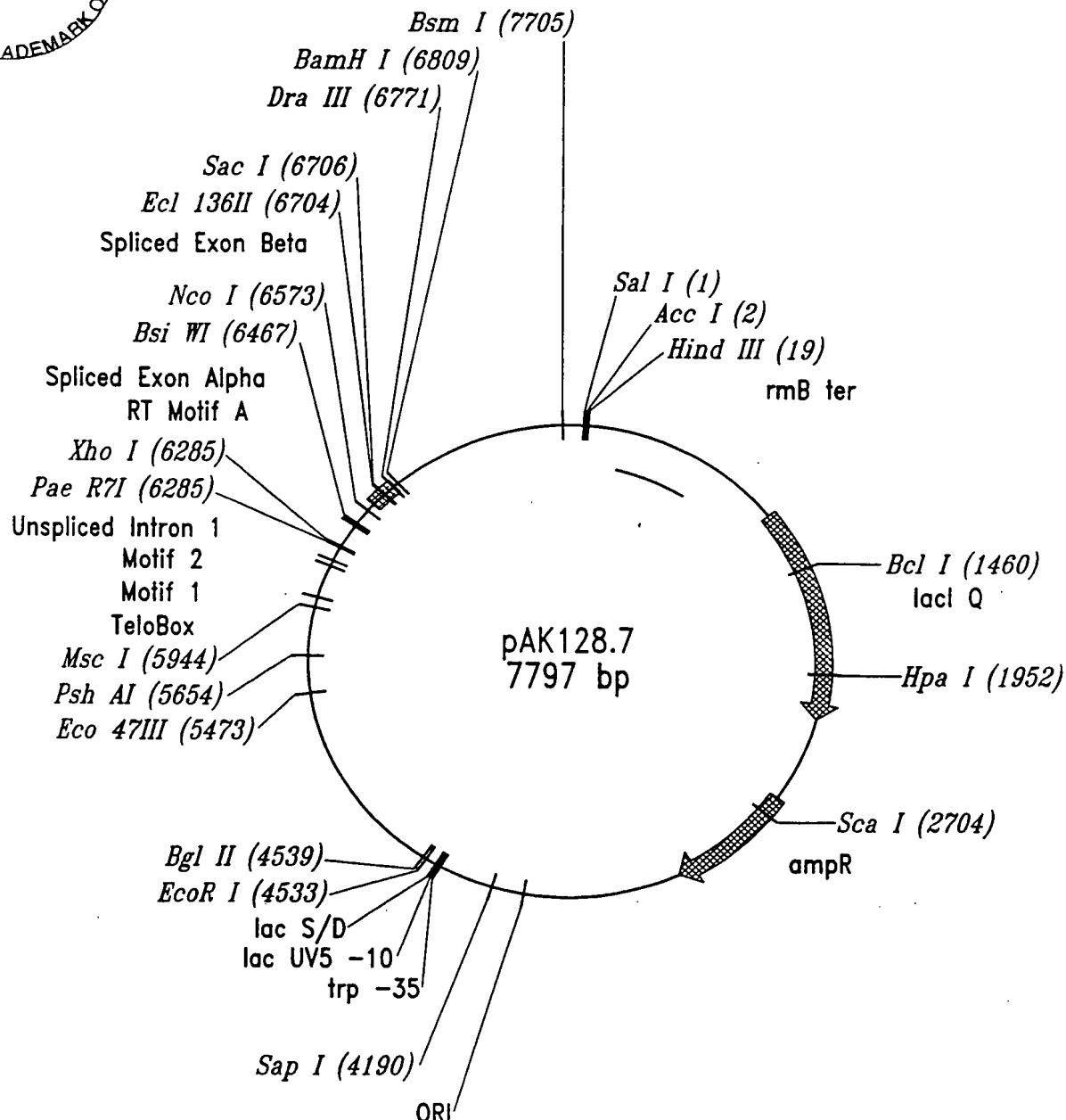


Fig. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular
DEFINITION Human telomerase clone with alternative C-terminus

Fig. 14B



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5521 cggccgttgc tggccgttgc cccatccatc cggccgttgc gggccgttgc

Fig. 14C



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Fig. 14D

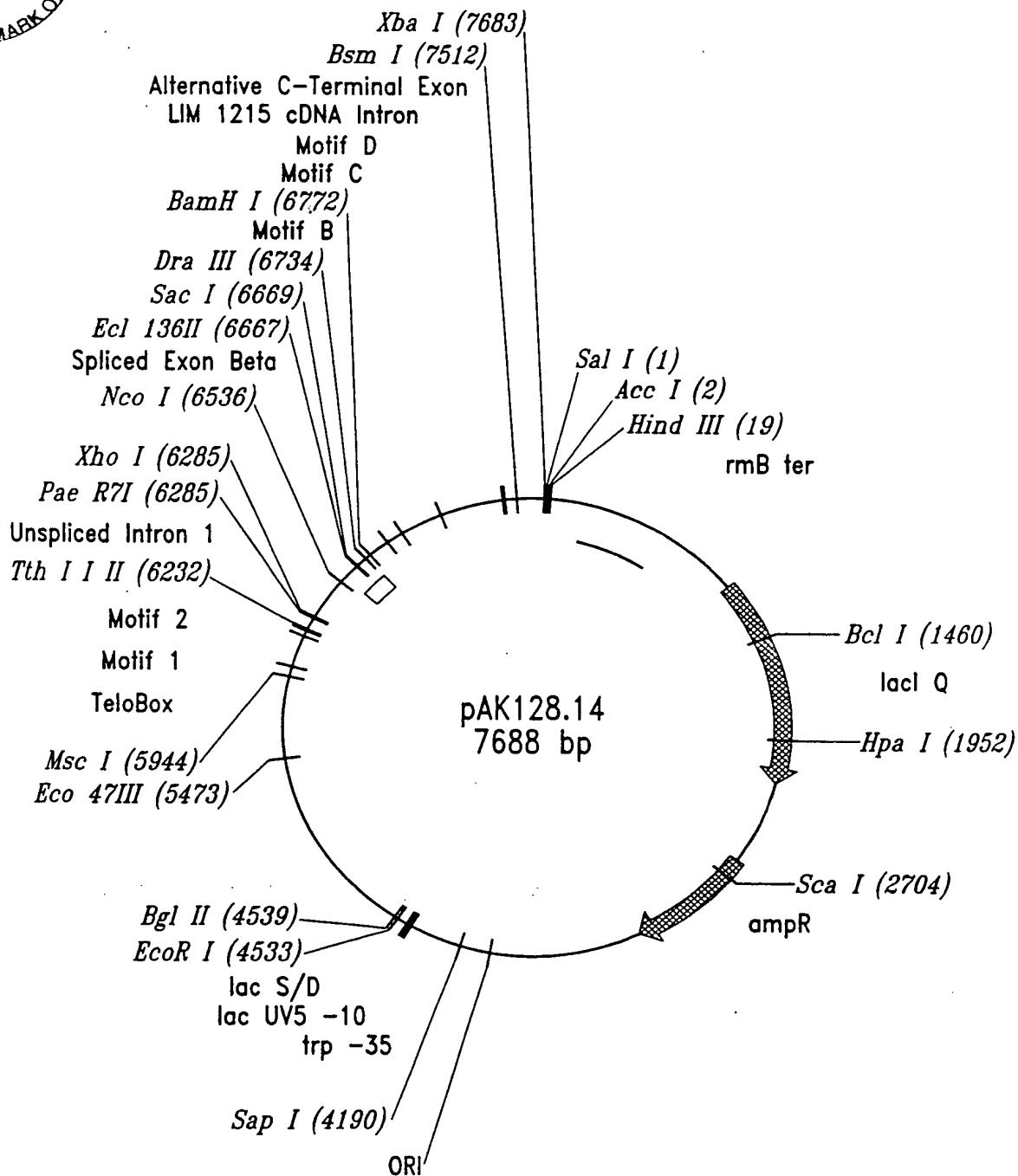


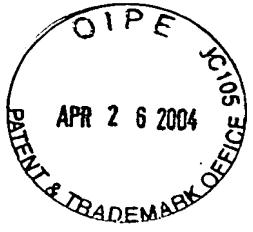
Fig. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular
DEFINITION Human telomerase clone with exon alpha spliced out

A circular stamp with the text "OIPE" at the top and "JC '05" at the bottom. The center contains the date "APR 26 2004". The outer border of the stamp contains the text "PATENT & TRADEMARK OFFICE".

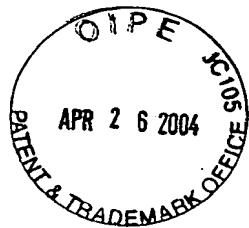
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Fig. 15B



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Fig. 15C



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Fig. 15D

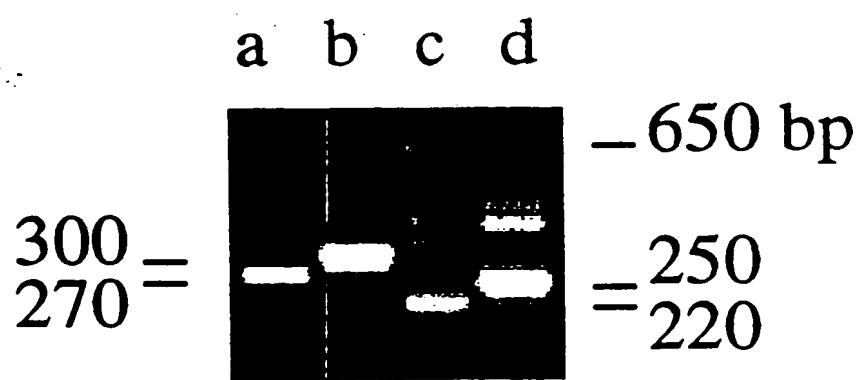


Fig. 9



sequence "Y" 104-105 bases

GGCCTCCCCGGGGTCGGCGTCCGGCTGGGTTGAGGGCGCCGGGGGAACCAAG
GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln
AlaSerProGlySerAlaSerGlyTrpGly* GlyArgProGlyGlyThrSer
ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCGCAGGTG
ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg
AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly
ThrCysGlyGluGlnArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTGTTAACCTCCTTTAACAGAA
ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "α" 36 bases

GTGGATGTGACGGGCGCGTACGACACCATCCCCAG
ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "β" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGCTCACCTG
ValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTACAGAGCTCCCTG
GlnGluThrSerProLeuArgAspAlaValIleGluGlnSerSerLeu

AATGAGGCCAGCAGTGGCCTTCTCGACGTCTCCTACGCTTCATGTGCCACCAC
AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA
AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGCAGGTGCTGCAG
Ter

GGCGTGTGCGTCCACCTCTGCTTCCGTGTGGGCAGGCAGTCCAATCCAAAGGGT
CAGATGCCACAGGGTGCCCTCGTCCATCTGGGCTGAGCACAAATGCATCTTCTG
TGGGAGTGAGGGTGCCCTACAACGGGAGCAGTTCTGTGCTATTTGGTAA...

Fig. 10A



sequence "3" 159 bases

CGAAGAAAACATTCTGCGTGAECTCCTGCGGTGCTTGGTGGGACAGCCAGAG
AlaGluGluAsnIleSerValValThrProAlaValLeuGlySerGlyGlnProGlu

ATGGAGCCACCCCGCAGACCGTCGGGTGTGGCAGCTTCCGGTGTCTCTGGGAGG
MetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg

GGAGTTGGGCTGGGCCTGTGAECTCCTCAGCCTCTGTTTCCCCAG
GlyValGlyLeuGlyLeu *

sequence "X" unknown length

...GACAGTCACCAGGGGGGTTGACCGCCGGACTGGCGTCCCCAGGGTTGACTATAGGA
CCAGGTGTCCAGGTGCCCTGCAAGTAGAGGGCTCTCAGAGGCCTGGCTGGCATGG
GTGGACGTGGCCCCGGGCATGGCCTCTGCGTGTGCCGTGGTGCCTGAGCCCT
CACTGAGTCGGTGGGGCTTGTGGCTCCCGTGAAGCTTCCCCTAGTCTGTTGTCTGG
CTGAGCAAGCCTCCTGAGGGCTCTATTG

partial sequence of genomic intron (approximately 2.7 kb)
GTGGCTGTGCTTGGTTAACCTCCTTTAACCAAGAAGTGCCTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGAGGAGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCACCCATTGTGCGCACAGTGAGGTGGCGAGGTGCCGTGCCTCCA
GAAAAGCAGCGTGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....

Fig. 10B



Truncated telomerase

ATGCCGCGCCTCCCGCTGCCGAGCCGTGCCCTCCGTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCACGTCGTG
 M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

 CGGCGCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCCTGGTGTGGCTGCCCTGGACGCACGGCGCCCCCGCGC
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

 CCCCTCCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCCGAGTGCAGAGGCTGTGCAGCGCGCGCGAAGAACGTGCTGGCCTCGGCTGCCCTGGACGGCGCCCCCGCG
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D O G A R

 CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACGCGGGGAGCGGGCGTGGGCGCTGCTGCCCTGGCGACGACGT
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

 GCTGGTTCACCTGCTGGCACGCTGCCGCTTTGTGCTGGTGGCTCCAGCTGCCCTACAGGTGTGCGGGCCCGCGTGTACAGCTGGCGCTGCCACTCAGGCCGGCCCCCGC
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

 ACACGCTAGTGGACCCGAAGGCCTGGGATGCAACGGCGTGGGACCGAACATAGCGTCAGGGAGGCCGGTCCCTGGGCTGCCAGCCGGTGCAGAGGAGGCCGGCAGTGC
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

 CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGCGTGGCCTGCCCTGAGCCGAGCCGGACCCGGTGGCAGGGGCTGGCCACCCGGCAGGACCGTGGACCGAGTGC
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

 TGGTTCTGTGGTGTACCTGCCAGACCCCGCAAGAACGCCACCTCTTGGAGGGTGCCTCTGGCACCGCCTCCACCCATCCGTGGCCCGCAGCACACGCCGGCCCC
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

 ATCCACATCGGGCCACCGTCCCTGGACACGCCCTGGTACGCCAGACCAAGCTCTCTACTCCCTAGGCAGAACGGAGCAGCTGCCCTCTCCACTCAG
 S T S R P P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

 CCTCTGAGGCCAGCTGACTGGCCTGGAGGCTCGTGGAGACCACTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGCCTGCCAGCCTACTGGCA
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

 ATGGGGCCCTGTTCTGGAGCTGGAAACCACGCCAGTGGCCCTACGGGTGCTCTCAAGACGCACTGCCCTGGAGCTGCCAGGGTGCCTGCCAGCCTACTGGCA
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

 GGAGAAGCCCCAGGGCTGTGGCCGCCAGGCCAGGGAGGAGGACACAGACCCCGTCGCTGGCAGCTCCAGGCCAGCACAGCAGGCCCTGGAGGTGACGGCTCGTGGCC
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

 CCTGGCCGGCTGGTGGCCAGGCCCTGGGCTCCAGGCACAACGAACGCCGTTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCAGGAGC
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

 GACGTGGAAGATGAGCGTGGGGACTGCGCTGGCTGCCAGGAGCCAGGGTGGCTGTGTTCCGGCCAGAGCACCGCTGCCAGGGAGATCCTGGCAAGTTCCTGCACGGCT
 T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

 GATGAGTGTGACGCTGAGCTGCTCAGGTCTTCTTATGTACGGAGACACGTTCAAAAGAACAGGTCTTTCTACCGGAAGAGTGTGGAGCAAGTGGCAAGGATTGG
 M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

 AAT--NNN--GACAGTCACCGGGGTTGACCGCCGGACTGGCGTCCCCAGGGTTGACTATAGGACCAAGGTGCTGCCCTGCAAGTAGAGGGCTCTAGAGGCCTGGCTGG

Fig. 11A



CATGGGTGGACGTGGCCCCGGGATGGCCTCTGCCGTGCTGCCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGCTTGTGGCTCCCGTGAGCTTCCCCTAGTCTGTGCTG

GCTGAGCAAGCCTCCTGAGGGGCTCTATTG..

Fig. 11B



Truncated protein 1

ATGCCGCAGCTCCCCCTGCCAGCCGTGCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGCCACGTC
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGGCCGGGACCCGGCGCTTCCCGCGCTGGTGCCAGTGCTGCCCTGGTGCCTGGCTGCCCTGGACGCACGCCGCCCGCC
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCTCTTCCGCCAGGTCTGCCTGAAGGAGCTGGTGCCAGTGCTGCAGAGCTGTGCAGGCCAGCTGGCTGCCCTGGCTGCCCTGGACGCACGCCGCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCCCGAGGCCTTACCAACAGCGCTGCCAGCTACCTGCCAACACGGTGAACGACGCACTGCCGGGAGCGGGCGTGGGGCTGCTGCTGCCGCCGTGGCGACGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACCTGCTGGCACGCTGCCGCTTTGTGGCTCCAGCTGCCCTACAGGTGCGGGCCGCCGCTGCTACAGCTGCCGCTGCCACTCAGGCCGCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGCGTCTGGATGCAACGGCCTGGAACCATAGCTCAGGGAGGCCGGTCCCTGGCTGCCACGCCGGTGCAGGAGGCCGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAACAGGCCAGGCCGCTGCCCTGAGCCGGACGCCGTTGGCAGGGCTCTGGCCACCCGGCAGGACGCCGCTGGACCGAGTGCACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTTGTCACCTGCCAGACCCGCCAGAGACCCGCCAGAGAACCCCTTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGGCCGCCAGCACACGCCGCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACACGCTCCCTGGACACGCCCTGTCCCCCGTGTACGCCAGACCAAGCACTTCTACTCCCTCAGGCCACAAGGAGCAGCTGCCCTCTTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCCACTGACTGCCGCTGGAGGCTCGTGGAGACCATTTCTGGGTCCAGGCCCTGGATGCCAGGGACTCCCCCAGGTTGCCCTGCCAGGCCACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y H Q

AATGGGGCCCTGTTCTGGAGCTGCTGGAACCAAGGCCACTGCCCTACGGGTCTCTCAAGACGCACTGCCGCTGGAGCTGCCCTACCCAGCAGGGTGTCTGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

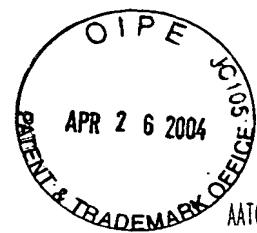
GGAGAAGGCCAGGGCTGTGGCGGCCAGGGAGGAGGAGACAGACCCCGTCGCTGGTGCAGCTGCCAGCACGCCCTGGCAGGTGACGGCTGTGCC
E K P Q G S V A A P E E E D T D P R R L V O L L R O H S S P W Q V Y G F V R A C

CCTGCCGGCTGGTGGCCCTGCCAGGCCACAAGCAACGCCCTGGTCTCCAGGAACACCAAGAAGTTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGGCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCGTCTGGTGAAGGAGATCTGGCAAGTCTGCC
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTACGTCGAGCTGCTCAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCTTTCTACCGGAAGAGTGTCTGGAGCAAGTGC
M S V Y V V E L L R S F F Y V T E T T F O K N R L F F Y R K S V W S K L Q S I G

Fig. 11C



AATCAGACAGCACTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAAGCAGAGGTAGGCAGCATCGGGAAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTTGGTTAACCTCCCTTTAACCGAGAA
V A V L W F T F L F N Q K

CGGGCTGCGGCCGATTGTGAACATGGACTACGTGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCAGCGTCTCACCTCGAGGGTAAGGCACTGTTAGCGTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G *

Fig. 11D



Truncated protein 2

ATGCCGGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCCTGGCACGTTGTG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGGACCCGGCGCTTCCGCGCGTGGTGGCCAGTGCTGTGCTGCCCTGGACGCACGGCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTTCCCGCAGGTGCTCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGGGCTGTGCAGCGCGCCGAAGAACGTGCTGCCCTGGCTCGCCTGCGCTGCGACGGGCCCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTTACCAACAGCGTGGCAGCTACCTGCCAACACGGTACCGGACTGCCGGGAGCGGGCGTGGGGCTGCTGCGCCGCTGGGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGGCTCTTGCTGGCTCCAGCTGCCTACCAAGGTGCTGGCCGCTGTACAGCTCGGCTGCCACTCAGGCCGGCTGCGACGGCCGGCCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGACCCGAAGGCGTCTGGATGCGAACGGCTGGAACCATAGCGTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCCCGGTGCAGGGAGGCCGGCAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCCTGCCAACAGGGCCAGGGCTGGCTGCCACTCCACCGTGGCCAGGGAGGCCGGTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCGCCAGAACAGCCACCTCTTGAGGGTGGCTCTGGACGCCACTCCACCCATCCGGGGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R O H H A G P P

ATCCACATCGCCGCCACCACGTCCCTGGACACGCCCTGTCCCCGGTACGCCAGACCAAGCACTTCTACTCTCAGGCAGAACGGAGCAGTGCAGGCCCTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTAGGCCAGCTGACTGGCTCGGAGGCTGGAGACCATCTTCTGGGCTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGCAGGCCCTGCCAGGCCACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACACAGCGCAGTCCCTACGGGTGCTCTCAAGACCAACTGCCGCTGCCAGCTGCCAGGCCAGGCCAGGCCAGGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

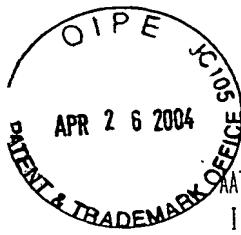
GGAGAAGCCAGGGCTGTGGCGCCCCAGGGAGGGAGACAGACCCCGCTGGCTGGACGCCAGCAGGCCCTGGCAGGTGACGGCTCGTGGCC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGGCTGGTCCCCCAGGCCCTGGGCTCCAGGCACAAGAACGCCCTCTCAGGAACACCAAGAACGATCTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGGGACTGCGCTGGCTGCCAGGAGCCAGGGTTGGCTGTTCCGGCCAGAGCACCGTGCCTGAGGAGATCTGGCAAGTCTCGCTGCCAGGAGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTCGAGCTGCTCAGGTCTTCTTGTACGGAGACCAAGCTTCAAAAGAACGGCTTACCGGAAGAGTGTCTGGAGCAAGTTGCAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L O S I G

Fig. 11E



ATCAGACAGCACTGAAGAGGGTCCAGCTGGGGAGCTGTCGAAGAGGTCAAGCACATCGGAAGCCAGGGCCCTGCTGACGTCCAGACTCCGCTTCATCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGGGCCATTGTGAACATGGACTACGTCGTCGGAGCCAGAACGTTCCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTAAGGCAGTGTTCAGCGTGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGCGGGCCCCGGCTCTGGGCCCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTTCGTCGCTGCGTGTGGGCCCCAGGACCCGGCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAGGTGGATGTGACGGCGGTACGACACCATCCCCAGGACAGGCTACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGCCGTGCGTCGGTATGCCGTGGTCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCCGCCATGGCACGTCGCCAAGGCCTTCAAGAGCCAC
K A A H G H V R K A F K S H

GTCTACGTCAGTG
V L R P V

CGAGGGATCCGCAGGGCTCCATCCTCCACGCTCTGAGCCTGTGCTACGGCACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCCTGG
P G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F G G
TGATTCTTGTGGTGACACCTCACCTACCCACGCAGAACCTTCAGGACCTGGTCCAGGTGCTCTGAGTATGGCTGCGGTGAATTGCGGAAGACAGTGGTAATTCCC
*



Reference protein

ATGCCGCGCTCCCCCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCTGCGGGCGCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
CGCGGGGACCCGGCGCTTCCGCGCCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGG	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
GACGCACGGCCGCCCGCCCGCCCTCCTCCGCCAGGTGTCCTGCCTGAAGGAGCTG	240
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
GTGGCCCAGTGCTGCAGAGGCTGTGCGAGCGCGGGCGAAGAACGTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGGACGGGCCCAGGGGGCCCCGAGGGCCTTCACCACCGCGTGC	360
PheAlaLeuLeuAspGlyAlaArgGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCAACACGGTGACCGACGCCTGCGGGGGAGCGGGGCGTGGGGCTGCTG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCTGGCGACGACGTGCTGGTTACCTGCTGGCACGCTGCGCCTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGTGTACCAGCTGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCGGCCCCGCCACACGCTAGTGGACCCCGAAGGCGTGGGATGCGAA	600
AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgLeuGlyCysGlu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGGCCTGCCAGCCCCGGT	660
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
GCGAGGAGGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGGCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
GGCGCTGCCCTGAGCCGGAGCGGACGCCGTTGGCAGGGGTCTGGGCCACCCGGC	780
GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACCGCTGGACCGAGTGACCGTGGTTCTGTGTTGTCACCTGCCAGACCCGCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
GAAGCCACCTTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGC	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300

Fig. 11G



CGCCAGCACACGCCGGCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCC ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	960 320
TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCCACAAGGAGCAG CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	1020 340
CTGCCGCCCTCCTCCTACTCAGCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTC LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	1080 360
GTGGAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCC ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	1140 380
CGCCTGCCCGCGCTACTGGCAAATGCCGCCCTGTTCTGGAGCTGCTGGAAACCAC ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuGlyAsnHis	1200 400
GCGCAGTGCCCTACGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGTCACC AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	1260 420
CCAGCAGCCGGTGTCTGTGCCCGGGAGAACGCCCCAGGGCTCTGTGGCGGCCCGAGGAG ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	1320 440
GAGGACACAGACCCCCGTCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCGGCAG GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	1380 460
GTGTACGGCTTCGTGGGGCCTGCCTGCGCCGGCTGGTGCCTGGGGCTCTGGGGCTCC ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	1440 480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAACGTTCATCTCCCTGGGAAGCAT ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	1500 500
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGGCTGCGCTTGGCTG AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	1560 520
CGCAGGAGCCCAGGGTTGGCTGTGTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGGTCTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
TTTTATGTCACGGAGACCACGTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTC PheTyrValThrGluThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal	1740 580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTGAAGAGGGTGCAGCTGCC TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTGGAAAGCAGAGGTCAAGGCAGCATTGGGAAGGCCAGGCCCTGCTGACGTCCAGA LeuSerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArg	1860 620

Fig. 11H



CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
GGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCA GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	1980 660
CTGTTCAGCGTGTCAACTACGAGCGGGCGCGCGCCCCGGCCTCCTGGCGCCTCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	2040 680
CTGGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGTGCGTGTGCGGGCCAG LeuGlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGln	2100 700
GACCCGCCGCCTGAGCTGTACTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATC. AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTCACGGAGGTACGCCAGCATCATCAAACCCCAGAACACGTACTGC ProGlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCys	2220 740
GTGCGTCGGTATGCCGTGGTCCAGAAGGCCGCCATGGGCACGTCCGCAAGGCCTTCAAG ValArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLys	2280 760
AGCCACGTCTCACCTTGACAGACCTCAGCCGTACATGCGACAGTTGTGGCTCACCTG SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	2340 780
CAGGAGACCAGCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAG GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTTCGACGTCTTACGCTTACGCTTACGCTTACGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	2520 840
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAGCTGTTGGGGATTGGCGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	2580 860
GGGCTGCTCCTCGGTTGGATGATTCTTGTGGTACACCTCACCTCACCCACGCG GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	2640 880
AAAACCTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTG LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	2700 900
CGGAAGACAGTGGTGAACCTCCCTGTAGAACGAGACGAGGCCCTGGTGGCACGGCTTTGTT ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	2760 920
CAGATGCCGGCCACGGCCTATTCCCTGGTGCAGGCCTGCTGCTGGATACCCGGACCTG GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuAspThrArgThrLeu	2820 940

Fig. 11I



GAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTC GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	2880 960
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTTTGGGTCTTGC GGCTG AsnArgGlyPheLysAlaGlyArgAsnMetArgArgLysLeuPheGlyValLeuArgLeu	2940 980
AAGTGTACAGCCTGTTCTGGATTTGCAGGTGAAACAGCCTCAGACGGTGTGCACCAAC LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	3000 1000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTCACGCATGTGTGCTGCAGCTCCA IleTyrLysIleLeuLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	3060 1020
TTTCATCAGCAAGTTTGGAGAGAACCCACATTTTCTGCGCGTCATCTGACACGGCC PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAla	3120 1040
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATTCGCTGGGGCCAAGGGC SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	3180 1060
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTC AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	3240 1080
AAGCTGACTCGACACCGTGTACCTACGTGCCACTCCTGGGTCACTCAGGACAGCCCAG LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	3300 1100
ACGCAGCTGAGTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAAAC ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	3360 1120
CGGGCACTGCCCTCAGACTCAAGACCATCCTGGAC ProAlaLeuProSerAspPheLysThrIleLeuAsp	3420 1132



Truncated protein 3

ATGCCGCGCCTCCCCCTGCCAGCCGTGCCCTCCGTGCCACCCACTACCGGAGGTGCTGCCCTGCCACCTTCGT
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGGCCCTGGGGCCCAGGGCTGGCGCTGGTCAAGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCCGCCAGGTGCTCCGTGAAGGAGCTGGTGGCCAGTGCTGAGAGGCTGTGCGAGCGCGCCGAAGAACGTCGCTGGCTTCGGCTGCTGGACGGGGCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACCGCGTCCGAGCTACCTGCCAACACGGTACCGACGCAGTGGGGAGCGGGGCTGCTGCTGCCCTGGCGTGGGACGAGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACGCTGGCCTCTTGCTGGCTCCAGCTGCCCTACCAAGGTGCGGGCCGCGCTGTACAGCTGGCGCTGCCACTCAGGCCGGCCCCCG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGGGACCCGAAGCGCTGGGATGCGAACGGCCTGGAACCATAGCGTCAGGGAGGCCGGTCCCTGGCCTGCCAGCCCCGGTGCAGGAGGGCCGGGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R R G G S A

CAGCCGAAGTCTGCCCTGCCAACAGAGGCCAGGCCTGGCGCTGCCCTGAGCCGGAGGCCGTTGGCAGGGTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGACCCCGAACAGAGGCCAGGCCTGGCGCTCTGGAGGGTGGCTCTGGCACGCCACTCCACCCATGGCCGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGCGGCCACCACGCCCTGGACACGCCCTGGTCCCCGGTGTACCGGAGACCAAGCCTCTACTCCCTAGCGACAAGGAGCAGTCGGCCCTCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGGAGACCATCTTCTGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGGTGGCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGGAACACGCCAGTGCCAGTCCCCCTACGGGTGCTCTCAAGACGACTGCCGTCGAGCTGGTCACCCAGCACGCCGTCTGTGCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

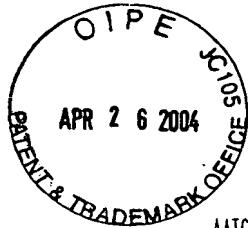
GGAGAAGGCCAGGGCTCTGGCGGCCAGGGAGGACACAGACCCCGTCGCTGGAGACCATCTGGTCCAGGCCCTGGAGGTGCTGCCAGCACGCCCTGGAGGTGCTGGC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGCTGGTGCCTGCCAGGCCCTGGCTCCAGGCACAACGAACGCCCTCCAGGAACACCAAGAAGTCACTCCCTGGGAAGCATGCCAGCTCGCTGCCAGGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAAGATGAGCGTGCAGGACTGCCCTGGCTGCCAGGAGCCCAGGGTGGCTGTTCCGGCCAGAGCACCGTCTGCCTGAGGAGATCTGGCAAGTCTGCACGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGCGCTGAGCTGCTCAGGTCTTCTTATGTCACGGAGACCAAGCTTCAAAGAACAGGCTCTTCTACCGGAAGAGTGTGCTGGAGCAAGTTGCAAGCATTGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11K



AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGTCGAAGCAGAGTCAGGCAGCATGGGAAGCCAGGCCCCCTGCTGACGTCCAGACTCCCTCATCCCCAAGCCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGCCGCCATTGTGAACATGGACTACGTCGTTGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCAGGGTCTCACCTCGAGGGTGAAGGCAGTGTCAAGCGTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGCGCCGCCGCCCTCTGGGCCCTCTGTGCTGGCCTGGACGATATCCACAGGGCCTGGCGCACCTCGTGCCTGCGTGTGCGGCCAGGACCCGCCCTGAGCTGTACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAGGTGGATGTGACGGCCGCTACGACACCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTCGTGCCTCGTATGCCGTGGTCCA
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P O N T Y C V R R Y A V V Q
GAAGGCCGCCATGGCACGTCGCCAAGGCCATGAGCACGTCACCTTGACAGACCTCCAGCCGTACATGGCACAGTTCTGCGTACCTGCAGGAGACCAGCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGTCGTATCGAGCAGAGCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGCTTCTACGCTTATGTGCCACACGCCGTGCATCAGGGCAAGTCCATGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCGCAGGGCTCCATCTCCACGCTCTGCAGCCTGTGCTACGGCAGATGGAGAACAGCTGTTGGGGATTGGCGGGACGGGCTGCTCCGTTGGTGG
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D
TGATTTCTTGTGGTACACCTCACCTACCCACGCAGAACCTCTCAGGACCTGGTCCGAGGTGCTCTGAGTATGGCTGGTGAACCTGCGAAGACAGTGGTGAACCTCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGTAGAAGACGAGGCCCTGGTGGCACGGCTTGTCAAGATGCCGCCACGGCTATTCCCTGGCGCCCTGCTGCTGGATACCGGACCCGGAGGTGCAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R
GTGAGCCACCTGGCCGAAGTGGAGCCGTGCCCCGCTGGGCAGGTGCTGCAGGGCCCTTGGTCCACCTCTGCTTCCGTGGGGCAGGCAGTGCCTGGAAATCCCCAAGGGTCAGA
*
TCCCACAGGGTCCCCCTGTCCTGAGCACAAATGCATTTCTGTTGAGGTGAGGTGCCTCACACGGAGCACTTTCTGCTTGGTAA...



Altered C-terminus protein

ATGCCGCCGCTCCCCGCTGCCAGCCGTGCCCTCCCTGCCAGCCACTACCGCAGGTGCTGCCCTGGCACCTCGT
 M P R A P R C R A V R S L L R S H Y R E V L P L A T E V

 CGGCCCTGGGCCCCAGGGCTGGCGCTGGTCAGCGGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCTGGACGACGGCCGCCCCGGCG
 R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

 CCCCTCTCCGCCAGGTGCTGCCTGAAGGAGCTGGTGGCCAGTGCTGAGAGCTGTGCGAGCGCCGCGAAGAACGTCGCTGGCTTCGCGCTGCGCTGGACGGGCG
 P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

 CGGGGGCCCCCGAGGCCTCACCAACAGCTGCGAGCTACCTGCCAACACGGTACCGACGCAGTGCAGGGGAGCGGGCGTGGGGCTGCTGCGCCCGTGGCGACGACGT
 G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

 GCTGGTTACCTGCTGGCACGCTGCGCTCTTGCTGGCTCCAGCTGCCAACAGGTGCGGGCCGCGTGTACCAAGCTCGCCGCTGCCACTCAGGCCGGCCCCCGCC
 L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

 ACACGCTAGTGGACCCGAAGGCCTGGGATGCCAACGGCCTGGAACCATAGCCTAGGGAGGCCGGTCCCGTGGCCAGGCCGGGTGCGAGGCCGGTGCAGGAGCGCGGGGAGTGC
 H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

 CAGCCGAAGTCTGCCGTGCCAACAGGGCCAGGGCTGGCGCTGCCCTGAGCCGGAGCGCCTGGCAGGGTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGCACCG
 S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

 TGGTTCTGTGTGGTGTACCTGCCAGACCCGCCAGAACGCCACCTCTTGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTTGGCCGCCAGCACACGCCGGCCCC
 G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

 ATCCACATGCCGCCACACGCCCTGGACACGCCCTTGCTGCCAGGCCACTCCCTACTCTCAGGCAGAAGGAGCAGCTGCCCTCCCTACTCAG
 S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

 CTCTGAGGCCAGCTGCTGGCGCTGGAGGCTGTGGAGACCATCTTGAGGGTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCCTGCCAGCGTACTGGCA
 S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

 AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTGCCTACGGGTGCTCTCAAGACGCACTGCCGCTGCCAGCTGCCACCCAGCAGCCGGTCTGTGCCCG
 M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

 GGAGAAGCCCCAGGGCTGTGGCGGCCCGAGGGAGGGACACAGACCCCGTCCCTGGTCAGCTGCCAGCACAGCAGGCCCTGGCAGGTGACGGCTCGTGCAGGAGCT
 E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

 CCTGCCGCCGCTGGTGCCTCCAGGCCCTGGGCTCCAGGCACAACGAAACGCCCTCCCTCAGGAACACCAAGAAGTCATCTCCCTGGGAAGCATGCCAAGCTCGCTGCAGGAGCT
 L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

 GACGTGGAAAGATGAGCGTGCAGGACTGCGCTGGCTGCGCAGGAGGCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCGCTGCGTGAAGGAGATCTGGCAAGTCCCTGCACTGGCT
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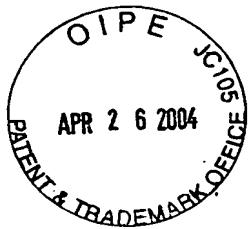
 GATGAGTGTGACGTGCTCGAGCTGCTCAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTGC
 M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11M



AATCAGACAGCACTTGAAGAGGGTGCAGCTGGGAGCTGCGGAAGCAGAGGTCAAGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCAGACTCGCTTCATCCCCAAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGGGGCGATTGTGAACATGGACTACGTGCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTTCAGCGTGC
G L R P I V N M O Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GCGGGCGGGCGCCCGGCCCTCTGGGCCTCTGTGCTGGGCTGGACGATATCCACAGGGCTGGCGACCTCGTGCCTGGGTGCGGCCCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAGGTGGATGTGACGGGCGGTACGACCCATCCCCAGGACAGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGGTATGCCGTT
V K V D V T G A Y D T I P Q D R L T E V I A S I I K P O N T Y C V R R Y A V V Q
GAAGGCCGCCATGGGACGTCCGCAAGGCCCTCAAGAGCCACGTCTACCTGACAGACCTCCAGCCGACATGCCGACAGTTCTGGCTCACCTGCAGGAGACCAGCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGCTCGTATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGTCTACGCTCATGTGCCACCACGCCGTCGCATCAGGGCAAGTCCTACGTCAGTG
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGGATCCGAGGGCTCCATCCTCTCCACCTGCTGCAGCTGTGCTACGGGACATGGAGAACAGCTGTTGGGGGATTGGGGGACGGCTGCTCTGCCTGGT
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D
TGATTTCTTGGTGAACACCTCACCTCACCCACCGAAAACCTCTCAGGACCTGGTCCGAGGTGTCCTGAGTATGGCTGGTGAACCTGGGAAGAACAGTGGTGA
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGAGAAGACGAGGCCCTGGTGGCACGGCTTTGTTAGATGCCGCCACGGCTATTCCCTGGTGGCCTGCTGCTGGATACCGGACCCCTGGAGGTGAGAGCGACTACTCCAG
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S
CTATGCCGCCACCTCCATCAGAGCCAGTCTCACCTCAACCGCGCTCAAGGCTGGGAGGAACATGCCGAAACTCTTGGGTCTGGCTGAAGTGTACAGCTGTTCTGG
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D
TTTGCAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAAGATCCTCTGCTGCAGGGTACAGTTCACTGCTGCTGCAGCTCCATTCTACAGCAAGTTGGAAAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N
CCCCACATTCTCGCGCTCATCTGACACGGCTCCCTCTGCTACTCCATCTGAAAGCCAAGAACGAGGGATGCGCTGGGGCAAGGGCGCCGCCCTGCTCCCTCGA
P T F F L R V I S D T A S L C Y S I L K A K N A E
|
CCGAAGAAAACATTCTGCTGACTCCTGGGTGCTGGTC
E E N I L V V T P A V L G S
GGGACAGCCAGAGATGGAGCCACCCGCAAGACCGTGGGTGTGGCAGCTTCCGGTGTCTCTGGAGGGAGTTGGCTGGCTGTGACTCCTAGCCTCTGTTCCCCAG
G Q P E M E P P R R P S G V G S F P V S P G R G V G L G L *

Fig. 11N



Protein that lacks motif A

APR 26 2004

ATGCCGGCGCTCCCCGCTGCCAGGCCGTGCGCTCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCACGTCGGCACGCCGCCGCC
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGGTGGTGCAGCGGGGGACCCGGCGCTTCCGCGCTGGTGCCCCAGTGCCTGGTGTGCGTGCCCTGGACGCACGCCGCCGCC
R R L G P Q G H R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCTCCGCCAGGGTGTCTGCCTGAAGGAGCTGGTGGCCCAGTGCAGAGGCTGTGCAGGCCGGCGAAGAACGTCGGCTTCGCCCTGGACGCCGCCGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTACCGCACGCACTGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCTGGCGTGGCGACGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACGCTGCCGCTTTGTGCTGGCTCCAGCTGCCAACAGGTGCGGGCCCGCTGTACAGCTGCCCTGCCACTCAGGCCGGCGACG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGGGACCCGAAGGGCTGGATGCGAACGGCTGGGCTGGACGGCCATAGCTCAGGGAGGCCGGTCCCCCTGGGCTGCCAGCCCCGGTGCAGGAGGCCGGGGCAGTC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTTGCCAACAGGGCCAGGGCTGGCTGCCCTGAGCCGGAGGCCGGACGCCCTGGGAGGGTCTGGGCTGCCAGCCCCGGCAGGACGCCGGTGGACCGAGTC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTTGTCACCTGCCAGACCCGCCAGAACGCCACCTTGGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGGCCGCCAGCACACGCCGGCCCC
G F C V V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

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S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCCATCTGGGCTGCCCTGAGGCCACTCCGGGCTGCCACGCCACTCCGGCCAGGTGCCCCCTGCCAGCGCTACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAAACACGCCAGTCCCTGAGGCCACTCCGGGCTGCCACGCCACTGCCGCTGCCAGGTGCCCCAGCAGCGTCTGTGCC
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

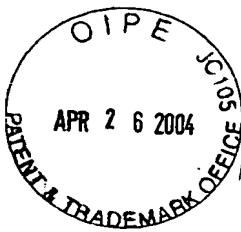
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E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTCCCCCAGGCCCTGGGCTCCAGGACACAGACCCCGTCCGGCTGGCAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGGCTTCGTGCC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAGATGAGCGTGCAGCTGGCTGCCAGGAGCCAGGGTTGGCTGTGCTGCCAGGAGGCCAGGAGCTGCCAGGAGATCTGGCAAGCTCGCTGCCAGGAGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGTCAGCTGGCTGCCAGGAGCTGGCTGCCAGGAGGCCAGGAGCTGGCTGTGCTGCCAGGAGGCCAGGAGATCTGGCAAGCTCGCTGCCAGGAGCT
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 110



AATCAGACAGCACTGAAAGGGTGAGCTGCCGGAGCTGTCGAAGCAGAGGTAGGCAGCATCGGAAGCCAGGCCCCCTGCTGACGTCAGACTCCCTCATCCCCAAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D
CGGGCTGGGGCGATTGTGAACATGGACTACGTCTGGAGCCAGAACCTCCGAGAGAAAAGAGGCCAGGGCTCCTACCTCGAGGGTGAAGGCAGTGTCAAGCTGCTCAACTACGA
G L R P I V N M O Y V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E
GGGGCGGGCGCCCTCTGGGCCTCTGTGCTGGCCTGGACATATCCACAGGGCTGGCGACCTCTGCTGGGTGCGGGCCAGGACCCGCCGCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F
TGTCAAG GAGGGCTACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGGTATGCCGTGGTCCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q
GAAGGCCCATGGCACGTCCCAAGGCCACGCTCTACCTGACAGACCTCCAGCCGACATGCCAGACTGGAGACAGTCTGCTGGCTACCTGCAGGAGACCAGCCGCTGAGGG
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D
TGCGTCGTCATCGAGCAGACCTCTCCCTGAATGAGGCCAGCAGTGGCTTCTGACGCTTCTACGCTCATGTGCCACACGCCGTCGCGCATCAGGGCAAGTCTACGTCAGT
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C
CCAGGGATCCGCAGGGCTCCATCTCTCCACGCTGCTGAGGACATGGAGAACAGCTGTTGGGGATTGGGGGCTGCTCTGCCTGGTGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L R L V D
TGATTCTTGTGGTACACCTCACCCACGCAGAACCTCTCAGGACCTGGTCCGAGGTGCTGAGTATGGCTGCGTGGTGAACITGCGGAAGACAGTGGTGAACITCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P
TGTAGAAGACGAGGCCCTGGTGGCACGGCTTTGTCAGATGCCGCCACGCCATTCCCTGGTCCGAGGTGCTGAGTATGGCTGCGTGGTGAACITGCGGAAGACAGTGGTGAACITCCC
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S S
CTATGCCGCACCTCCATCAGAGCCAGTCTCACCTCAACGCCGCTCAAGGCTGGAGGAACATGCCGAAACTCTTGGGTCTTGCCTGAAGTGTCAAGCTGTTCTGGA
Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L D
TTGCAGGTAAACAGCTCAGACGGTGTGACCAACATCTACAAGATCTCTGCTGAGGCTACAGTTACGCATGTCGCTGAGCTCCATTCAAGCAAGTTGGAGAA
L Q V N S L Q T V C T N I Y K I L L L Q A Y R F H A C V L Q L P F H Q Q V W K N
CCCCACATTTCTGCCGTATCTGACACGCCCTCCCTGCTACTCCATCTGAAAGCAAGACGCCAGGGATGTCGCTGGGGCAAGGGCGCCGCGCCCTGCCCC
P T F F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P S E
GGCGTGCAGTGGCTGCCCCAACAGCATTCTGCTCAAGCTGACTCGACACGGTGTACCTACGCTGCCACTCCTGGGTACTCAGGACAGCCAGCCAGCTGAGTCGGAAGCTCC
A V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P
GGGACGACCTGACTGCCCTGGAGGCCAGCCAACCCGGCACTGCCCTGAGCTCAAGACCATCTGGACTCATGCCACCCGCCACAGCCAGGGAGAGCAGACCCAGCC
G T T L T A L E A A A N P A L P S D F K T I L D
CTGTCACGCCGGCTCACGTCCAGGGAGGGGGGGCCACACCGAGGCCACCGCTGGAGCTGAGGCTGAGTGTGAGTGTGTTGGCCAGGGCTGCATGCGCTGAAGGCT
GAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACTGCCCTTCACTCCCCACAGGCTGGCGCTGGCTCCACCCAGGGCAGCTTCCAC
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Fig. 11P



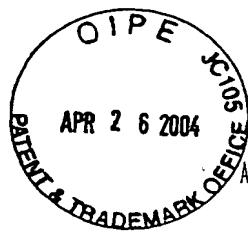
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AATACTGAATATATGAGTTTCAGTTTGAA

Fig. 11Q



Truncated protein that lacks motif A

Fig. 11R



AATCAGACAGCACTGAAGAGGGTCAGCTGCGGAGCTGCGGAAGCAGAGGTCAAGCAGCATGGAGCCAGGCCCCTGCTGACGTCCAGACTCCGCTCATCCAAAGGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

CGGGCTCGGGCGATGTGAACATGGACTACGTCCTGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCAGTTCACTACGA
G L R P I V N M O V V G A R T F R R E K R A E R L T S R V K A L F S V L N Y E

GCGGGCGCGCCGGCCCTCTGGGCGCTCTGTGCTGGGCCTGGACGATATCCACAGGGCTGGCGCACCTCGTGCTGCGTGTGCGGGCCAGGACCCGCCCTGAGCTGACTT
R A R R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y F

TGTCAAG GACAGGCTCACGGAGGTATGCCAGCATCATCAAACCCAGAACACGTACTGCGTGCCTGCGTATGCCGTGGTCA
V K D R L T E V I A S I I K P Q N T Y C V R R Y A V V Q

GAAGGCGCCATGGCACGTCCCAAGGCCACGCTCTACCTTGACAGACCTCCAGCGTACATGCGACAGTTGCTCACCTGCAAGGAGACCAAGCCGCTGAGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D

TGCGTGTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTCGACGCTTCCACGCTCATGTCGACCCACGCCGTGCATCAGGGCAAGTC
A V V I E Q S S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C

CCAGGGATCCCGAGGGCTCCATCTCCACGCTGCTGAGCTACGGGACATGGAGAACAGCTGTTGCGGGATTGGCGGGACGGCTGCTCTGCGTTGGGA
Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L L R L V D

TGATTTCTGTGGTACACCTCACCCACCGAAAACCTCTCAGGACCTGGTCCAGGTGCTCTGAGTATGGCTGCGTGTGAACCTGCGGAAGACAGTGGTGA
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F P

TGAGAAAGACGAGGCCCTGGGTGGCACGGCTTTGTTAGATGCCGCCACGGCTATTCCCTGGTGGCGCTGCTGCTGAGTACCCGGACCCCTGGAGGTCA
V E D E A L G G T A F V Q M P A H G L F P W C G L L L D T R T L E V Q S D Y S R

GTGAGCCACCTGGCCGAAGTGGAGCCTGTGCCCCGCTGGGCAGGTGCTGCAGGGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGCAGGCAGT
* GCAATCCAAAGGGTCAGA

TGCCACAGGGTGGCCCTCGTCCATCTGGGCTGAGCACAAATGCATTTCTGTGGAGTGGGGTGCCTCACACGGAGCAGTTCTGTGTATTTGGTAA

Fig. 11S



Lacks motif A and altered C-terminus

ATGCCGCGCGCTCCCGCTGCCGAGCCGCTGCCCTGCTGCCAGCCACTACCGCGAGGTGCTGCCCTGGCACGCCACGGCCGCCCGCCG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGCCCCAGGGCTGGCGCTGGTGCAGCGGGACCCGGCGCTTCCGCGCTGGTGGCCAGTGCCTGGTGTGCCTGCCCTGGACGCCACGGCCGCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

CCCCCTCCGCCAGGTGCTCTGAAGGAGCTGGTGGCCAGTGCAGAGGCTGTGCAGGCCGCGCAAGAACGCTGGCTTCGGCTCGCCTGGACGCCGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCGGGGGCTTACCCAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGGAGCGGGCGTGGGGCTGCTGCTGCCGCCGCTGGACGCC
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACTGCTGGCACGCTGGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGTGCCGCTGCTACCGCTGCCACTGCCACTCAGGCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGACCCGAAGGGCTGGATGCCAACGGGCTGGAACCATAGCGTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGGCCGGGTGCCACTCAGGCCGCC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCCTGCCAACAGGCCAGGGCTGGCCTGCCCTGAGCGAGGCCGGTGGCAGGGGCTGGCCACCCGGCAGGACGGTGGACCGAGTGCACCG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTTCTGTGGTGTACCTGCCAGACCCGCCAGAACAGCCACCTTGGAGGGTGGCTCTGCCACGGCCACTCCACCCATCGTGGCCGCCAGCACCCAGGCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

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S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGCCGCCCTGTTCTGGAGCTGCTGGAACACGCCAGTCCCTACGGGCTGCCCAAGACGACTGCCGCTGCCAGCTGCCAGGCC
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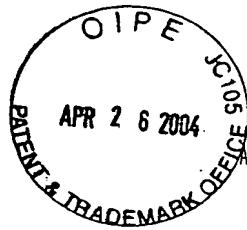
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CTCTGCCGGCTGGGCCCTCAGGCCTGGGCTCCAGGCACAACGACCCGCTCTCAGGAACACCAAGAAGTCATCCCTGGGAAGCATGCCAGCTCGCTGCC
L R R L V P P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

GACGTGGAAAGATGAGCGTGGACTGCCCTGGCTGCCAGGAGCCAGGGTTGGCTGTGTTCCGGCCAGAGCACCCTGCGTGGAGATCTGGCAAGTCTGCTGCC
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L

GATGAGTGTGACGTGCTGAGCTGCTAGGTCTTCTTATGTCAGGAGACCAAGCTTCAAAAGAACAGGCTTCTACCGGAAGAGTGTGAGCAAGTGC
M S V Y V V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G

Fig. 11T



ATCACACAGCACTTGAAGAGGGTGCAGCTGGGGAGCTGCGAACAGAGGTAGGGAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCAGACTCCGTTCATCCCCAACCTGA
 IRQHLKRVQLRELSEAEVROHREARPALLTSRLRFIPKPD
 CGGGCTGCCGCGATTGTGACATGGACTACGTGTTGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTAGCGTGCCTAACACGA
 GLRPIVNMODYVVGARTFRREKRAERLTSRVKALFSVLYE
 GCGGGCGGCCGCCGCCGCCCTCTGGCGCCTGTGCTGGCCCTGGACGATATCACACAGGGCCTGGCGACCTTCGTCGCTGCGTGTGCGGCCAGGACCCCCCCTGAGCTGACTT
 RARRPGLLGASVLGLDDIHRAWRTFVLRVRAQDPPELYF
 TGTCAGG
 VK
 GACAGGCTCACGGAGTCATGCCAGCATCATCAAACCCAGAACACGTAACGCTGCGTGCCTGCGTGCCTGAGGACAGCCGCTGAGGG
 DRLTEVIASIICKPQNTYCVRRYAVVO
 GAAGGCCGCCATGGCACGTCGCAAGGCCACGCTCTCACCTGACAGACCTCCAGCGTACATGCGACAGTCGTCGCTCACCTGAGGAGACCAGCCGCTGAGGG
 KAAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLQETSPLRD
 TGCGCTGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAGCAGTGGCTCTTCGACGCTTCACGCTCATGTGCCACACGCCGTGCGCATAGGGCAAGTCCTACGTCAGTG
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 FGVLRLKCHSFLD
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 FHQVQVWKN
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 PTFFLRVISDTASLCYSILKAKNAE
 CCGAAGAAACATTCTGCTGACTCTGCGTGCTGGT
 EENILVVTPTPAVLGS
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 GQPEMEEP
 PRRPSGVGS
 F
 P
 V
 S
 P
 G
 R
 G
 V
 G
 L
 G
 L
 *

Fig. 11U



Truncated telomerase (ver. 2)

ATGCCGCGCGCTCCCGCTGCCAGCGCTCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGGCACGCGCCACGTCGT
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCCTGGGCCAGGGCTGGCGCTGGTCAGCGCGGACCCGGCGCTTCCCGCGCTGGCCAGTGCCTGGTGTGGCTGCCCTGGGACGCACGGCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCGGGTCCGGCTGGGTGAGGGCGCCGGGAACCGCGACATGCCAGCGACTCAGGGCGCTCCCCCGAGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCTCCTCCGCCAGGTCTCTGCCTGAAGGAGCTGGTGGCCAGTGCTGCAGAGGCTGTGCAGGCCGGCGCGAAGAACGTGCTGGCCTGGCTTGCGCTGGACGGGCCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

GGGGGCCCCCGAGGCCCTCACCAACAGCGTGCAGCTACCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGGCTGCTGCCTGGCGTGGACGGACG
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTCACCTGCTGGCACGCTGGCTCTTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCGCCGCTGTACAGCTGGCGCTGCCACTCAGGGCGCTGGACGGCCG
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGGGACCCGAAGGGCTGGATGCAACGGCGCTGGACCCAGCTGGCCCTGGCACGGAGGGCTGGCGCTGGCCAGCCGGGTGCGAGGGCGGGAGTG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGCTGCCGTGCCCAAGAGGCCAGGGCTGGCCCTGCCCTGAGCCGAGGCCGCTGGCAGGGCTGGCCACCCGGCAGGACCGTGGACCGAGTG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGTGGTGTACCTGCCAGACCCCGAAGAACCCACCTTGGAGGGTGCCTCTGGCACGCCACTCCACCCATCCGTGGCCGCCACCCACGCCGG
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

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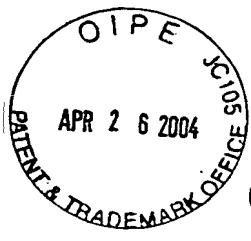
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M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCAGGGCTGTGGCGGCCAGGGAGGAGGACACAGACCCCGTGCCTGGAGCTGCCAGACAGGCCCTGGCAGGGTACGGCTGCG
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCCGCCCTGGTGGCCAGGCCTGGGCTCCAGGCACAACGAACGCCCTCCAGGAACCAAGAAGTCATCCCTGGGAAGCATGCCAAGCTCGCTGCCAGGAGC
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11V



GACGTGGAAGATGAGCGTGCAGGGACTGCGCTGGCTGCGCAGGGAGCCAGGGGTTGGCTGTTCCGGCGCAGAGCACCGTCTCGTGAGGAGATCCTGGCCAAGTTCTGACTGGCT
T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L
GATGAGTGTGACGTGTCGAGCTGCTCAGGTCTTCTTTATGTACGGAGACCAAGCTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
AAT--NNN--GACAGTCACCAGGGGGTTGACCGCCGGACTGGGCTCCCAGGGTTGACTATAGGACAGGTGTCCAGGTGCCCTGCAAGTAGAGGGCTCTAGGGCTGGCTGG
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GCTGAGCAAGCCTCCTGAGGGCTCTATTG...

Fig. 11W



Truncated protein 1 (ver. 2)

ATGCCCGCGCTCCCCGCTGCCGAGCCGTGCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGGCACGTCG
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGCGCGCTGGGGCCCAGGGCTGGCGGCTGGTGCAGCGCGGGACCCGGCGCTTCCCGCGCTGGTGGCCAGTGCCTGGTGCCTGGCACGGACGGCCACGGCGCCCCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCTCCCCGGGTCCGGTCCGGCTGGGTTGAGGGCGCCGGGGAAACAGCGACATGCCAGAGCAGCGCAGCGACTCAGGGCGCTTCCCCCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P O V

CCCCCTCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCAGAGGCTGTGCAGCGCGCGAAGAACGTGCTGGCTTCGCCCTCGCCTGCTGGACGGGCC
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACCGCTGCCAGCTACCTGCCAACACGGTGACCGACGCACTCGGGGGAGCGGGCGTGGGGCTGCTGCTGCCCTGCGCCTGGGACACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTACCTGCTGGCACCGCTGCCGCTTTGCTGGCTCCAGCTGCCCTACAGGTGCGGGCCCGCCGCTGACAGCTGCCACTCAGGGCCGGCCCCGCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTCTGGGATGCAACGGCTGGGAACCATAGCGTCAGGGAGGCCGGTCCCGCTGCCAGCCCCGGTGCAGGGAGGCCGGCAGTGC
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGCCAGGGCTGGCGCTGCCCTGAGCCGAGCCGGTGGCAGGGCTCTGGCCAGGGCTCTGGCCACCCGGCAGGACGCGTGGACCGAGTGC
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTTGCTCACCTGCCAGACCCGCCAGAGAACGCCACTCTTGAGGGTGCCTCTGCCACCGCCACTCCACCCATCCCTGGCCGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATGCCGCCACCGCTCCCTGGACACGCCCTGCCCCGGTACGCCAGACCAAGCCTCTACTCCCTAGGCACAAGGAGCAGCTGCCCTCTTCACTCG
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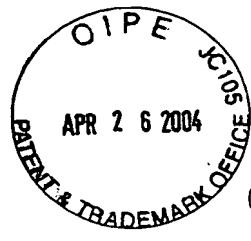
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M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

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Fig. 11X

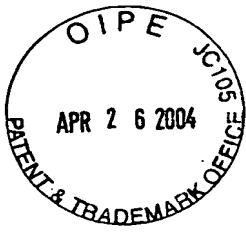


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GATGAGTGCTACGTGTCGAGCTGCTCAGGTCTTCTTTATGTCACGGAGACCAAGCTTCAAAGAACAGGCTCTTCTACCGGAAGGTGCTGGAGCAAGTTGCAAAGCATGG
M S V Y V V E L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G
AATCAGACAGCACTTGAAAGAGGGTGCAGCTGCGGGAGCTGCGGAAGCAGAGGTCAAGCAGCATCGGAAGCCAGGCCGCTGCTACGTCAGACTCCGCTCATCCCCAAGCTGA
I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D

GTGGCTGTGCTTGGTTAACCTCCCTTTAACAGAA
V A V L W F T F L F N Q K

CGGGCTGCGCCGATTGTGAACATGGACTACGTGCGGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTAGCAGCTCAACTACGA
G L R P I V N M D Y V V G A R T F R R E K R P S V S F R G *

Fig. 11Y



Truncated protein 2 (ver. 2)

ATGCCGCCGCTCCCCCTGCCAGCCGTGCCCTCCCTGCTGCCAGCCACTACCCGAGGTGCTGCCCTGCCACGTTGTC
M P R A P R C R A V R S L L R S H Y R E V L P L A T F V

CGGCGCCTGGGGCCCCAGGGCTGGCGCTGGTGACCGCGGGGACCCGGCGCTTCCGCCGCTGGTGGCCAGTGCTGGTGTGCCGCCGGGACGCCACGGCCGCCCCCGCCG
R R L G P Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A

GGCCTCCCCGGGTGGCGTCCGGCTGGGTTGAGGGCGGCGGGGGACCAGCAGCATGCCAGAGCAGCAGCCAGGCACTCAGGGCGCTCCCCCGAGGTG
G L P G V G V R L G L R A A G G N O R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

CCCCCTCCGCCAGGTGCTCTGCCGAAGGAGCTGGTGGCCAGTGCTGCCAGAGGTGCTGCCAGGCGCGAGAACGTGCTGGCCTCGGCCCTGCCGTGCTGGACGGGCG
P S F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A F G F A L L D G A R

CGGGGGCCCCCGAGGCCTCACCAACCGTGCGCAGCTACCTGCCAACACGGTACCGACCGACTGCCGGGGAGCGGGCGTGGGGCTGCTGCCGTGGCGACGACGT
G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V

GCTGGTTCACCTGCTGGCACCGCTGCCGCTTTGCTGGCTCCAGCTGCCCTACCGGTGCTGCCAGCTCGGGCCGCCGCTGTACAGCTGCCGTGCCACTCAGGCCGGCCCC
L V H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P P

ACACGCTAGTGGACCCGAAGGGCTCTGGGATCGAACGGGCTGGAACCATAGCCTCAGGGAGGCCGGTCCCCCTGGCCTGCCAGCCGGTGCAGGAGGCCGGAGTG
H A S G P R R R L G C E R A W N H S V R E A G V P L G L P A P G A R R R G G S A

CAGCCGAAGTCTGCCGTGCCAACAGGCCAGGGCTGGCGTCCCCTGAGCCGGAGCCGGCCTGGGCAAGGGCTGGGCCACCCGGCAGGACCGTGGACCGAGTG
S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R

TGGTTCTGTGGTGTACCTGCCAGCCGCCAACAGGCCACTTGGAGGGTGCCTCTGCCACGCCACTCCACCCATCCGTGGCCGCCAGCACACGCCGGCCCC
G F C V V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P

ATCCACATCGGGCCACCACGCTCCCTGGACACGCCCTGCCCCGGTACGCCAGACCAAGCCTCCCTACTCCTCAGGCACAAGGAGCAGCTGCCCTCCCTACTCAG
S T S R P P R P W D T P C P P V Y A E T K H F L Y S S G D K E Q L R P S F L L S

CTCTCTGAGGCCAGCTGACTGGCGCTGGAGGCTGTGGAGACCATCTTCTGGTTCCAGGCCCTGGATGCCAGGGACTCCCGCAGGTGCCCCCTGCCAGGCCACTGGCA
S L R P S L T G A R R L V E T I F L G S R P W M P G T P R R L P R L P Q R Y W Q

AATGGGGCCCTGTTCTGGAGCTGCTGGGAACCACGCCAGTCCCCACGGGGTCTCTCAAGACGCACTGCCGTGCGAGCTGCCAGCCAGGCCAGGTGCTGTGCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R

GGAGAAGCCCCAGGGCTCTGGCGGCCCGAGGGAGGGACACAGACCCCGTCGCCCTGGTCAGCTGCCAGCACAGCAGCCCTGGCAGGTGACGGCTCGTGC
E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C

CCTGCGCCGGCTGGTGCCTCAGGCACAACGAACGCCCTCTGGGAGCTCAGGAACACCAAGAAGTCACTCCCTGGGAAGCATGCCAGCTCGTGCAGGAGCT
L R R L V P P G L W G S R H N E R R F L R N T K K F I S L G K H A K L S L Q E L

Fig. 11Z